

## SEQUENCE LISTING

## (1) GENERAL INFORMATION

- (i) APPLICANT: Escobedo, Jaime  
Quianjin, Hu  
Garcia, Pablo  
Williams, Lewis T.  
Kothakota, Srinivas
- (ii) TITLE OF THE INVENTION: Secreted Human Proteins
- (iii) NUMBER OF SEQUENCES: 38
- (iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: Banner & Witcoff  
(B) STREET: 1001 G Street, NW  
(C) CITY: Washington  
(D) STATE: DC  
(E) COUNTRY: USA  
(F) ZIP: 20001
- (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Diskette  
(B) COMPUTER: IBM Compatible  
(C) OPERATING SYSTEM: DOS  
(D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER:  
(B) FILING DATE: 11-DEC-1997  
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: 60/032757  
(B) FILING DATE: 11-DEC-1996
- (viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: Kagan, Sarah A  
(B) REGISTRATION NUMBER: 32141  
(C) REFERENCE/DOCKET NUMBER: 2441.39505
- (ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: 202-508-9100  
(B) TELEFAX: 202-508-9299  
(C) TELEX:

## (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2063 base pairs

- (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GAATTCGGCA	CGAGGCCTCA	GTCTTCCAGG	GCGGCGGTGG	GTGTCCGCTT	CTCTCTGCTC	60
TTCGACTGCA	CCGCACTCGC	GCGTGACCCT	GACTCCCCCT	AGTCAGCTCA	GCGGTGCTGC	120
CATGGCGTGG	CGGCGGCGCG	AAGCCGGCGT	CGGGGCTCGC	GGCGTGTTGG	CTCTGGCGTT	180
GCTCGCCCTG	GCCCTGTGCG	TGCCCCGGGC	CCGGGGCCGG	GCTCTCGAGT	GGTTCTCGGC	240
CGTGGTAAAC	ATCGAGTACG	TGGACCCGCA	GACCAACCTG	ACGGTGTTGA	GCGTCTCGGA	300
GAGTGGCCGC	TTCGGCGACA	GCTCGCCCAA	GGAGGGCGCG	CATGGCCTGG	TGGGCGTCCC	360
GTGGGCGCCC	GGCGGAGACC	TCGAGGGCTG	CGCGCCCGAC	ACGCGCTTCT	TCGTGCCCGA	420
GCCCGGCGCC	CGAGGGGCGC	CGCCCTGGGT	CGCCCTGGTG	GCTCGTGGGG	GCTGCACCTT	480
CAAGGACAAG	GTGCTGGTGG	CGGCGCGGAG	GAACGCCTCG	GCCGTCGTCC	TCTACAATGA	540
GGAGCGCTAC	GGGAACATCA	CCTTGCCCAT	GTCTCACGCG	GGAACAGGAA	ATATAGTGGT	600
CATTATGATT	AGCTATCCAA	AAGGAAGAGA	AATTTTGGAG	CTGGTGCAAA	AAGGAATTCC	660
AGTAACGATG	ACCATAGGGG	TTGGCACCCG	GCATGTACAG	GAGTTCATCA	GCGGTCAGTC	720
TGTGGTGTTC	GTGGCCATTG	CCTTCATCAC	CATGATGATT	ATCTCGTTAG	CCTGGCTAAT	780
ATTTTACTAT	ATACAGCGTT	TCCTATATAC	TGGCTCTCAG	ATTGGAAGTC	AGAGCCATAG	840
AAAAGAACT	AAGAAAGTTA	TTGGCCAGCT	TCTACTTCAT	ACTGTAAAGC	ATGGAGAAAA	900
GGGAATTGAT	GTTGATGCTG	AAAATTGTGC	AGTGTGTATT	GAAAAATTCA	AAGTAAAGGA	960
TATTATTAGA	ATTCTGCCAT	GCAAGCATAT	TTTTTCATAGA	ATATGCATTG	ACCCATGGCT	1020
TTTGGATCAC	CGAACATGTC	CAATGTGTAA	ACTTGATGTC	ATCAAAGCCC	TAGGATATTG	1080
GGGAGAGCCT	GGGATGTAC	AGGAGATGCC	TGCTCCAGAA	TCTCCTCCTG	GAAGGGATCC	1140
AGCTGCAAAT	TTGAGTCTAG	CTTTACCAGA	TGATGACGGA	AGTGATGACA	GCAGTCCACC	1200
ATCAGCCTCC	CCTGCTGAAT	CTGAGCCACA	GTGTGATCCC	AGCTTTAAAG	GAGATGCAGG	1260
AGAAAATACG	GCATTGCTAG	AAGCCGGCAG	GAGTGA CTCT	CGGCATGGAG	GACCCATCTC	1320
CTAGCACACG	TGCCCCTGTA	AGTGGCACCA	ACAGAAGTTT	GGCTTGA ACT	AAAGGACATT	1380
TTATTTTTTT	TACTTTAGCA	CATAATTTGT	ATATTTGAAA	ATAATGTATA	TTATTTTACC	1440
TATTAGATTC	TGATTTGATA	TACAAAGGAC	TAAGATATTT	TCTTCTTGAA	GAGACTTTTC	1500
GATTAGTCCT	CATATATTTA	TCTACTAAAA	TAGAGTGTTT	ACCATGAACA	GTGTGTTGCT	1560
TCAGACTATT	ACAAAGACAA	CTGGGGCAGG	TACTCTAATA	TAAAGGACAG	GTGGTGT TTC	1620
TAAATAATTG	GCTGCTATGG	TTCTGTAAAA	ACCA GTTAAT	TCTATTTTTC	AAGGTTTTTG	1680
GCAAAGCACG	TCAATGTTAG	ACTAGTTGAA	GTGGAATTGT	ATAATTCAAT	TCGATAATTG	1740
ATCTCATGGG	CTTTCCCTGG	AGGAAAGGTT	TTTTTTGTTG	TTTTTTTTTT	AAGAACTTGA	1800
AACTTGTAAG	CTGAGATGTC	TGTAGCTTTT	TTGCCCATCT	GTAGTGTATG	TGAAGATTTC	1860
AAAACCTGAG	AGCACTTTTT	CTTTGTTTAG	AATTATGAGA	AAGGCACTAG	ATGACTTTAG	1920
GATTTGCATT	TTTCCCTTTA	TTGCCTCATT	TCTTGTGACG	CCTTGTTGGG	GAGGGAAATC	1980
TGTTTATTTT	TTCTACAAA	TAAAAAGCTA	AGATTCTATA	TCGCAAAAAA	AAAAAAAAAA	2040
AAAAAAAAAA	TTCTGCGGC	CGC				2063

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1328 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GAATTCGGCA	CGAGGTAGGC	AAGGGATAAA	AAGGCACCTA	AGGCCCTTTT	GCAATAAGAA	60
GCCAGATGGA	TAAAGGAAGT	GCTGGTCACC	CTGGAGGTGT	ACTGGTTTGG	GGAAGGTCCC	120

CGGCCCCCAC	AGCCCTCTGG	GGAGCCTCAC	CCTGGCTCTC	CCCACTCACC	TCAGCCCTCA	180
GGCAGCCCCCT	CCACAGGGCC	CCTCTCCTGC	CTGGACAGCT	CTGCTGGTCT	CCCCGTCCCC	240
TGGAGAAGAA	CAAGGCCATG	GGTCGGCCCC	TGCTGCTGCC	CCTGCTGCTC	CTGCTGCAGC	300
CGCCAGCATT	TCTGCAGCCT	GGTGGCTCCA	CAGGATCTGG	TCCAAGCTAC	CTTTATGGGG	360
TCACTCAACC	AAAACACCTC	TCAGCCTCCA	TGGGTGGCTC	TGTGGAAATC	CCCTTCTCCT	420
TCTATTACCC	CTGGGAGTTA	GCCATAGTTC	CCAACGTGAG	AATATCCTGG	AGACGGGGCC	480
ACTTCCACGG	GCAGTCCTTC	TACAGCACAA	GGCCGCCTTC	CATTCAACAAG	GATTATGTGA	540
ACCGGCTCTT	TCTGAACTGG	ACAGAGGGTC	AGGAGAGCGG	CTTCTCAGG	ATCTCAAACC	600
TGCGGAAGGA	GGACCAGTCT	GTGTATTTCT	GCCGAGTCGA	GCTGGACACC	CGGAGATCAG	660
GGAGGCAGCA	GTTGCAGTCC	ATCAAGGGGA	CCAAACTCAC	CATCACCCAG	GCTGTCACAA	720
CCACCACCAC	CTGGAGGGCC	AGCAGCACAA	CCACCATAGC	CGGCCTCAGG	GTCACAGAAA	780
GCAAAGGGCA	CTCAGAATCA	TGGCACCTAA	GTCTGGACAC	TGCCATCAGG	GTTGCATTGG	840
CTGTGCTGT	GCTCAAAACT	GTCATTTTGG	GACTGCTGTG	CCTCCTCCTC	CTGTGGTGGA	900
GGAGAAGGAA	AGGTAGCAGG	GCGCCAAGCA	GTGACTTCTG	ACCAACAGAG	TGTGGGGAGA	960
AGGGATGTGT	ATTAGCCCCG	GAGGACGTGA	TGTGAGACCC	GCTTGTGAGT	CCTCCACACT	1020
CGTTCCCCAT	TGGCAAGATA	CATGGAGAGC	ACCCTGAGGA	CCTTTAAAG	GCAAAGCCGC	1080
AAGGCAGAAG	GAGGCTGGGT	CCCTGAATCA	CCGACTGGAG	GAGAGTTACC	TACAAGAGCC	1140
TTCATCCAGG	AGCATCCACA	CTGCAATGAT	ATAGGAATGA	GGTCTGAACT	CCACTGAATT	1200
AAACCACTGG	CATTTGGGGG	CTGTTTATTA	TAGCAGTGCA	AAGAGTTCCT	TTATCCTCCC	1260
CAAGGATGGA	AAAATACAAT	TTATTTTGCT	TACCATAAAA	AAAAAAAAAA	AAAAATTCCT	1320
GCGGCCGC						1328

## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1689 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GAATTCGGCA	CGAGGGCAAG	ATTCGATACA	AAACCAATGA	ACCTGTGTGG	GAGGAAAAC	60
TCACTTTCTT	CATTCACAAT	CCCAAGCGCC	AGGACCTTGA	AGTTGAGGTC	AGAGACGAGC	120
AGCACCAGTG	TTCCCTGGGG	AACCTGAAGG	TCCCCCTCAG	CCAGCTGCTC	ACCAGTGAGG	180
ACATGACTTG	GAGCCAGCGC	TTCCAGCTCA	GTAACCTCGG	TCCAAACAGC	ACCATCAAGA	240
TGAAGATTGC	CCTGCGGGTG	CTCCATCTCG	AAAAGCGAGA	AAGGCCTCCA	GACCACCAAC	300
ACTCAGCTCA	AGTCAAACGT	CCCTCTGTGT	CCAAAGAGGG	GAGGAAAACA	TCCATCAAAT	360
CTCATATGTC	TGGGTCTCCA	GGCCCTGGTG	GCAGCAACAC	AGCTCCATCC	ACACCAGTCA	420
TTGGGGGCG	TGATAAGCCT	GGTATGGAAG	AAAAGGCCCA	GCCCCCTGAG	GCCGGCCCTC	480
AGGGGCTGCA	CGACCTGGGC	AGAAGCTCCT	CCAGCCTCCT	GGCCTCCCCA	GGCCACATCT	540
CAGTCAAGGA	GCCGACCCCC	AGCATCGCCT	CGGACATCTC	GCTGCCCATC	GCCACCCAGG	600
AGCTGCGGCA	AAGGCTGAGG	CAGCTGGAAA	ACGGGACGAC	CCTGGGACAG	TCTCCACTGG	660
GGCAGATCCA	GCTGACCATC	CGGCACAGCT	CGCAGAGAAA	CAAGCTTATC	GTGGTCGTGC	720
ATGCCTGCAG	AAACCTCATT	GCCTTCTCTG	AAGACGGCTC	TGACCCCTAT	GTCCGCATGT	780
ATTTATTACC	AGACAAGAGG	CGGTCAGGAA	GGAGGAAAAC	ACACGTGTCA	AAGAAAACAT	840
TAAATCCAGT	GTTTGATCAA	AGCTTTGATT	TCAGTGTTC	GTTACCAGAA	GTGCAGAGGA	900
GAACGCTCGA	CGTTGCCGTG	AAGAACAGTG	GCGGCTTCCT	GTCCAAAGAC	AAAGGGCTCC	960
TTGGCAAAGT	ATTGGTTGCT	CTGGCATCTG	AAGAACTTGC	CAAAGGCTGG	ACCCAGTGTT	1020
ATGACCTCAC	GGAAGATGGG	ACGAGGCCCT	AGGCGATGAC	ATAGCCGCAG	CAGGCAGGAG	1080
GCGTCTCTT	CAGCGTAGCT	CTCCACCTCT	ACCCGGAACA	CACCTCTCA	CAGACGTACC	1140
AATGTTATTT	TTATAATTTT	ATGGATTTAG	TTATACATAC	CTTAATAGTT	TTATAAAATT	1200
GTTGACATTT	CAGGCAAATT	TGGCCAATAT	TATCATTGAA	TTTTCTGTGT	TGGATTTCTT	1260
CTAGGATTTT	GCCAGTTTCT	ACAACGTGCA	GTAGGGCGGC	GGTAGCTCTT	GTGTCTGTGG	1320
ACTCTGCTCA	GCTGTGTCCG	TAGGAGTCGG	ATGTGTCTGT	GCTTTATTAT	GGCCTTGTTT	1380
ATATATCACT	GAGGTATACT	ATGCCATGTA	AATAGACTAT	TTTTTATAAT	CTTAACATGC	1440

TGGTTTAAAT	TCAGAAGGAA	ATAGATCAAG	GAAATATATA	TATTTTCTTC	TAAAACTTAT	1500
TAAATTCGTG	TGACAAATAA	TCATTTTCAT	CTTGGCAGCA	AAAAGTTCTC	AGTGACCTAT	1560
TTTGTGGTGT	TTCTTTTGA	AAAGAAAAGC	TGAAATATTA	TTAAATGCTA	GTATGTTTCT	1620
GCCCATTATG	AAAGATGAAA	TAAAGTATTC	AAAATATTAA	AAAAAAAAAA	AAAAAATTC	1680
TGCGGCCGC						1689

## (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1505 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GAATTCGGCA	CGAGGAGCAG	ATCTGCAAGA	GTTTCGTTTA	TGGAGGCTGC	TTGGGCAACA	60
AGAACAACATA	CCTTCGGGAA	GAAGAGTGCA	TTCTAGCCTG	TCGGGGTGTG	CAAGGTGGGC	120
CTTTGAGAGG	CAGCTCTGGG	GCTCAGGCGA	CTTTCCCCCA	GGGCCCCCTC	ATGGAAAGGC	180
GCCATCCAGT	GTGCTCTGGC	ACCTGTCAGC	CCACCCAGTT	CCGCTGCAGC	AATGGCTGCT	240
GCATCGACAG	TTTCCTGGAG	TGTGACGACA	CCCCCAACTG	CCCCGACGCC	TCCGACGAGG	300
CTGCCTGTGA	AAAATACACG	AGTGGCTTTG	ACGAGCTCCA	GCGCATCCAT	TTCCCCAGCG	360
ACAAAGGGCA	CTGCGTGGAC	CTGCCAGACA	CAGGACTCTG	CAAGGAGAGC	ATCCCCGCGCT	420
GGTACTACAA	CCCCTTCAGC	GAACACTGCG	CCCCTTTTAC	CTATGGTGGT	TGTTACGGCA	480
ACAAGAACAA	CTTTGAGGAA	GAGCAGCAGT	GCCTCGAGTC	TTGTCGCGGC	ATCTCCAAGA	540
AGGATGTGTT	TGGCCTGAGG	CGGGAAATCC	CCATTCCCAG	CACAGGCTCT	GTGGAGATGG	600
CTGTGCGAGT	GTTCCTGGTC	ATCTGCATTG	TGGTGGTGGT	AGCCATCTTG	GGTTACTGCT	660
TCTTCAAGAA	CCAGAGAAAAG	GACTTCCACG	GACACCACCA	CCACCCACCA	CCCACCCCTG	720
CCAGCTCCAC	TGTCTCCACT	ACCGAGGACA	CGGAGCACCT	GGTCTATAAC	CACACCACGC	780
GGCCCCCTCTG	AGCCTGGGTC	TCACCGGCTC	TCACCTGGCC	CTGCTTCCTG	CTTGCCAAGG	840
CAGAGGCCTG	GGCTGGGAAA	AACTTTGGAA	CCAGACTCTT	GCCTGTTTCC	CAGGCCCCACT	900
GTGCCTCAGA	GACCAGGGCT	CCAGCCCCCT	TTGGAGAAGT	CTCAGCTAAG	CTCACGTCCT	960
GAGAAAGCTC	AAAGGTTTGG	AAGGAGCAGA	AAACCCTTGG	GCCAGAAGTA	CCAGACTAGA	1020
TGGACCTGCC	TGCATAGGAG	TTTGGAGGAA	GTTGGAGTTT	TGTTTCTCT	GTTCAAAGCT	1080
GCCTGTCCCT	ACCCCATGGT	GCTAGGAAGA	GGAGTGGGGT	GGTGTCAGAC	CCTGGAGGCC	1140
CCAACCCTGT	CCTCCCAGC	TCCTCTTCCA	TGCTGTGCGC	CCAGGGCTGG	GAGGAAGGAC	1200
TTCCCTGTGT	AGTTTGTGCT	GTAAAGAGTT	GCTTTTGTG	TATTTAATGC	TGTGGCATGG	1260
GTGAAGAGGA	GGGAAGAGG	CCTGTTTGGC	CTCTCTATCC	TCTTTCCTC	TTCCCCCAAG	1320
ATTGAGCTCT	CTGCCCTTGA	TCAGCCCCAC	CCTGGCCTAG	ACCAGCAGAC	AGAGCCAGGA	1380
GAAGCTCAGC	TGCATTCCGC	AGCCCCCACC	CCCAAGGTTT	TCCAACATCA	CAGCCCAGCC	1440
CGCCCACTGG	GTAATAAAAG	TGGTTTGTGG	AAAAAAAAAA	AAAAAAAAAA	AAGTCCTGCG	1500
GCCGC						1505

## (2) INFORMATION FOR SEQ ID NO:5:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2002 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GAATTCGGCA	CGAGGGCCAT	GGCCGGGCTA	TCCCGCGGGT	CCGCGCGCGC	ACTGCTCGCC	60
GCCCTGCTGG	CGTCGACGCT	GTTGGCGCTG	CTCGTGTCTG	CCGCGCGGGG	TCGCGGCGGC	120

CGGGACCACG	GGGACTGGGA	CGAGGCCTCC	CGGCTGCCGC	CGCTACCACC	CCGCGAGGAC	180
GCGGCGCGCG	TGGCCCGCTT	CGTGACGCAC	GTCTCCGACT	GGGGCGCTCT	GGCCACCATC	240
TCCACGCTGG	AGGCGGTGCG	CGGCCGGCCC	TTGCGCGACG	TCCTCTCGCT	CAGCGACGGG	300
CCCCCGGGCG	CGGGCAGCGG	CGTGCCCTAT	TTCTACCTGA	GCCCGCTGCA	GCTCTCCGTG	360
AGCAACCTGC	AGGAGAATCC	ATATGCTACA	CTGACCATGA	CTTTGGCACA	GACCAACTTC	420
TGCAAGAAAC	ATGGATTTGA	TCCACAAAGT	CCCCTTTGTG	TTCACATAAT	GCTGTCAGGA	480
ACTGTGACCA	AGGTGAATGA	AACAGAAATG	GATATTGCAA	AGCATTCGTT	ATTCATTCTGA	540
CACCCTGAGA	TGAAAACCTG	GCCTTCCAGC	CATAATTGGT	TCTTTGCTAA	GTTGAATATA	600
ACCAATATCT	GGGTCTTGGA	CTACTTTGGT	GGACCAAAAA	TCGTGACACC	AGAAGAATAT	660
TATAATGTCA	CAGTTCAGTG	AAGCAGACTG	TGGTGAATTT	AGCAACACTT	ATGAAGTTTC	720
TTAAAGTGGC	TCATACACAC	TTAAAAGGCT	TAATGTTTCT	CTGGAAAGCG	TCCCAGAATA	780
TTAGCCAGTT	TTCTGTCACA	TGCTGGTTTG	TTTGCTTGCT	TGTTTACTTG	CTTGTTTACC	840
AATAGAGTTG	ACCTGTTATT	GGATTTCCCTG	GAAGATGTGG	TAGCTACTTT	TTTCCTATTT	900
TGAAGCCATT	TTCGTAGAGA	AATATCCTTC	ACTATAATCA	AATAAGTTTT	GTCCCATCAA	960
TTCCAAAGAT	GTTTCCAGTG	GTGCTCTTGA	AGAGGAATGA	GTACCAGTTT	TAAATTGCCC	1020
ATTGGCATT	GAAGGTAGTT	GAGTATGTGT	TCTTTATTCC	TAGAAGCCAC	TGTGCTTGGT	1080
AGAGTGCATC	ACTCACCACA	GCTGCCCTCT	GAGCTGCCTG	AGCCTGGTGC	AAAAGGATTG	1140
GCCCCCATTA	TGGTGCTTCT	GAATAAATCT	TGCCAAGATA	GACAAACAAT	GATGAAACTC	1200
AGATGGAGCT	TCTCATCAT	GTTGATTTAT	GTCTCACAAT	CCTGGGTATT	GTTAATTCAA	1260
CATAGGGTGA	AACTATTTCT	GATAAAGAAC	TTTTGAAAAA	CTTTTATAC	TCTAAAGTGA	1320
TACTCAGAAC	AAAAGAAAGT	CATAAACTC	CTGAATTTAA	TTTCCCCACC	TAAGTCGAGA	1380
CAGTATTATC	AAAACACATG	TGCACACAGA	TTATTTTTTG	GCTCCAAAAC	TGGATTGCAA	1440
AAGAAAGAGG	AGAGATATTT	TGTGTGTTCC	TGGTATTCTT	TTATAAGTAA	AGTTACCCAG	1500
GCATGGACCA	GCTTCAGCCA	GGGACAAAAT	CCCCTCCCAA	ACCACTCTCC	ACAGCTTTTT	1560
AAAAATACTT	CTACTCTTAA	CAATTACCTA	AGGTTCCTTC	AAACCCCCC	AACTCTTAAT	1620
AGCTTCTAGT	GCTGCTACAA	TCTAAGTCAG	GTCACCAGAG	GGAAGAGAAC	ATGGCATTA	1680
AAGAATCACA	TCTTCAGAAG	AGAAGACACT	AATATTATTA	CCCATATACA	TGATTTCAGA	1740
AGATGACATA	AGATTCTCT	TAAAGAGGAA	ATGTCAGGAA	TCAAGCCACT	GAATCCTTAA	1800
AGAGAAAAGT	TGAATATGAG	TCATTGTGTC	TGAAAAGTGC	AAAGTGAAGT	TAAGTGAGAT	1860
CCAGCAAACA	GGTCTGTTT	AAGAAAAATA	ATTTATACTA	AATTTAGTAA	AATGGACTTC	1920
TTATTCAAAG	CATCAATAAT	TAAAAGAAAT	ATTTTAAAAA	AAAAAATAAA	AAAAAATAAA	1980
AAAAAATAAT	TCCTGCGGCC	GC				2002

## (2) INFORMATION FOR SEQ ID NO:6:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1322 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GAATTCGGCA	CGAGGGCCAC	GACTCTGCTG	GCATTTCTTC	TATAGCCACT	GGAATCTGAT	60
CCTGATTGTC	TTCCACTACT	ACCAGGCCAT	CACCACTCCG	CCTGGGTACC	CACCCCAGGG	120
CAGGAATGAT	ATCGCCACCG	TCTCCATCTG	TAAGAAGTGC	ATTTACCCCA	AGCCAGCCCG	180
AACACACCAC	TGCAGCATCT	GCAACAGGTG	TGTGCTGAAG	ATGGATCACC	ACTGCCCCTG	240
GCTAAACAAT	TGTGTGGGCC	ACTATAACCA	TCGGTACTTC	TTCTCTTTCT	GCTTTTTTCAT	300
GACTCTGGGC	TGTGTCTACT	GCAGCTATGG	AAGTTGGGAC	CTTTTCCGGG	AGGCTTATGC	360
TGCCATTGAG	AAAATGAAAC	AGCTCGACAA	GAACAACTA	CAGGCGGTTG	CCAACCAGAC	420
TTATCACCAG	ACCCACCCAC	CCACCTTCTC	CTTTCGAGAA	AGGATGACTC	ACAAGAGTCT	480
TGCTTACCTC	TGGTTCCTGT	GCAGTTCGTG	GGCACTTGCC	CTGGGTGCC	TAAGTGATG	540
GCATGCTGTT	CTCATCAGTC	GAGGTGAGAC	TAGCATCGAA	AGGCACATCA	ACAAGAAGGA	600
GAGACGTCGG	CTACAGGCCA	AGGGCAGAGT	ATTTAGGAAT	CCTTACAAC	ACGGCTGCTT	660
GGACAACTGG	AAGGTATTCC	TGGGTGTGGA	TACAGGAAGG	CACTGGCTTA	CTCGGGTGCT	720
CTTACCTTCT	ACTCACTTGC	CCCATGGGAA	TGGAATGAGC	TGGGAGCCCC	CTCCCTGGGT	780

(2) INFORMATION FOR SEO ID NO:7:

(A) LENGTH: 1573 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

GAATTCGGCA	CGAGGAGCCT	GCCTTCATCT	AGGATGGCTC	CTCTGGGCAT	GCTGCTTGGG	60
CTGCTGATGG	CCGCCTGCTT	CACCTTCTGC	CTCAGTCATC	AGAACCTGAA	GGAGTTTGCC	120
CTGACCAACC	CAGAGAAGAG	CAGCACCAAA	GAAACAGAGA	GAAAAGAAAC	CAAAGCCGAG	180
GAGGAGCTGG	ATGCCGAAGT	CCTGGAGGTG	TCCACCCGA	CGCATGAGTG	GCAGGCCCTT	240
CAGCCAGGGC	AGGCTGTCCC	TGCAGGATCC	CACGTACGGC	TGAATCTTCA	GACTGGGGAA	300
AGAGAGGCAA	AACTCCAATA	TGAGGACAAG	TTCCGAAATA	ATTTGAAAGG	CAAAAGGCTG	360
GATATCAACA	CCAACACCTA	CACATCTCAG	GATCTCAAGA	GTGCACTGGC	AAAATTCAAG	420
GAGGGGGCAG	GAGATGGAGAG	TTCAAAGGAA	GACAAGGCAA	GGCAGGCTGA	GGTAAAGCGG	480
CTCTTCCGCC	CCATTGAGGA	ACTGAAGAAA	GACTTTGATG	AGCGAATGT	TGTCATTGAG	540
ACTGACATGC	AGATCATGGT	ACGGCTGATC	AACAAGTTCA	ATAGTTCCAG	CTCCAGTTTG	600
GAAGAGAAGA	TTGCTGCGCT	CTTTGATCTT	GAATATTATG	TCCATCAGAT	GGACAATGCG	660
CAGGACCTGC	TTTCTTTTGG	TGGTCTTCAA	GTGGTGATCA	ATGGGCTGAA	CAGCACAGAG	720
CCCCTCGTGA	AGGAGTATGC	TGCGTTTGTG	CTGGGCGCTG	CCTTTTCAG	CAACCCCAAG	780
GTCCAGGTGG	AGGCCATCGA	AGGGGGAGCC	CTGCAGAAGC	TGCTGGTCAT	CCTGGCCACG	840
GAGCAGCCGC	TCACTGCAA	GAAGAAGGTC	CTGTTTGCAC	TGTGCTCCCT	GCTGCGCCAC	900
TTCCCCTATG	CCCAGCGGA	GTTCTGAAG	CTCGGGGGGC	TGCAGGTCTT	GAGGACCTTG	960
GTGCAGGAGA	AGGGCAGCGA	GGTGCTCGCC	GTCGCGGTGG	TCACACTGCT	CTACGACCTG	1020
GTCACGGAGA	AGATGTTTCG	CGAGGAGGAG	GCTGAGCTGA	CCCAGGAGAT	GTCCCCAGAG	1080
AAGCTGCAGC	AGTATCGCCA	GGTACACCTC	CTGCCAGGCC	TGTGGGAACA	GGGCTGGTGC	1140
GAGATCACGG	CCCACCTCCT	GGCGCTGCCC	GAGCATGATG	CCCGTGAGAA	GGTGCTGCAG	1200
ACACTGGGCG	TCCTCCTGAC	CACCTGCCGG	GACCGCTACC	GTCAGGACCC	CCAGCTCGGC	1260
AGGACACTGG	CCAGCCTGCA	GGCTGAGTAC	CAGGTGCTGG	CCAGCCTGGA	GCTGCAGGAT	1320
GGTGAGGAGC	AGGGCTACTT	CCAGGAGCTG	CTGGGCTCTG	TCAACAGCTT	GCTGAAGGAG	1380
CTGAGATGAG	GCCCCACACC	AGGACTGGAC	TGGGATGCCG	CTAGTGAGGC	TGAGGGGTGC	1440
CAGCGTGGGT	GGGCTTCTCA	GGCAGGAGGA	CATCTTGCCA	GTGCTGGCTT	GGCCATTAAA	1500
TGGA AACCTG	AGGCCCAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	1560
TTCCTGCGGC	CGC					1573

(A) LENGTH: 1185 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GAATTCGGCA	CGAGGGGGCT	TTAAGGGACA	GCTGAGCCGG	CAGGTGGCAG	ATCAGATGTG	60
GCAGGCTGGG	AAAAGACAAG	CCTCCAGGGC	CTTCAGCTTG	TACGCCAACA	TCGACATCCT	120
CAGACCCTAC	TTTGATGTGG	AGCCTGCTCA	GGTGCGAAGC	AGGCTCCTGG	AGTCCATGAT	180
CCCTATCAAG	ATGGTCAACT	TCCCCCAGAA	AATTGCAGGT	GAACCTCTATG	GACCTCTCAT	240
GCTGGTCTTC	ACTCTGGTTG	CTATCCTACT	CCATGGGATG	AAGACGTCTG	ACACTATTAT	300
CCGGGAGGGC	ACCCTGATGG	GCACAGCCAT	TGGCACCTGC	TTCGGCTACT	GGCTGGGAGT	360
CTCATCCTTC	ATTTACTTCC	TTGCCTACCT	GTGCAACGCC	CAGATCACCA	TGCTGCAGAT	420
GTTGGCACTG	CTGGGCTATG	GCCTCTTTGG	GCATTGCATT	GTCCTGTTCA	TCACCTATAA	480
TATCCACCTC	CACGCCCTCT	TCTACCTCTT	CTGGCTGTTG	GTGGGTGGAC	TGTCCACACT	540
GCGCATGGTA	GCAGTGTGG	TGTCTCGGAC	CGTGGGCCCC	ACACAGCGGC	TGCTCCTCTG	600
TGGCACCCCTG	GCTGCCCTAC	ACATGCTCTT	CCTGCTCTAT	CTGCATTTTG	CCTACCACAA	660
AGTGGTAGAG	GGGATCCTGG	ACACACTGGA	GGGCCCCAAC	ATCCCGCCCA	TCCAGAGGGT	720
CCCCAGAGAC	ATCCCTGCCA	TGCTCCCTGC	TGCTCGGCTT	CCCACCACCG	TCCTCAACGC	780
CACAGCCAAA	GCTGTTGCGG	TGACCCTGCA	GTCACACTGA	CCCCACCTGA	AATTCTTGGC	840
CAGTCCTCTT	TCCCGCAGCT	GCAGAGAGGA	GGAAGACTAT	TAAAGGACAG	TCCTGATGAC	900
ATGTTTCGTA	GATGGGGTTT	GCAGCTGCCA	CTGAGCTGTA	GCTGCGTAAG	TACCTCCTTG	960
ATGCCTGTCTG	GCACCTCTGA	AAGGCACAAG	GCCAAGAACT	CCTGGCCAGG	ACTGCAAGGC	1020
TCTGCAGCCA	ATGCAGAAAA	TGGGTCAGCT	CCTTTGAGAA	CCCCTCCCCA	CCTACCCCTT	1080
CCTTCCTCTT	TATCTCTCCC	ACATTGTCTT	GCTAAATATA	GACTTGGTAA	TTAAAATGTT	1140
GATTGAAGTC	TGGAATAAAA	AAAAAAAAAA	AATTCCTGCG	GCCGC		1185

## (2) INFORMATION FOR SEQ ID NO:9:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1226 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GAATTCGGCA	CGAGGCAAGC	CACCATCTTC	CTTCGGCCTG	CACCCCTTTA	AAGGCACCCA	60
GACCCCTCTG	GAAAAAGATG	AACTGAAGCC	CTTTGACATC	CTCCAGCCTA	AGGAGTACTT	120
CCAGCTCAGC	CGCCACACGG	TCATTAAGAT	GGGAAGTGAG	AACGAGGCC	TGGATCTCTC	180
CATGAAGTCA	GTGCCCTGGC	TCAAGGCTGG	TGAAGTCAGT	CCCCCAATCT	TCCAGGAAGA	240
TGCAGCCCTA	GACCTGTCAG	TGGCAGCCCA	CCGGAAATCC	GAGCCTCCCC	CTGAGACACT	300
GTATGACAGT	GGTGCATCAG	TGGACAGCTC	AGGTCACACA	GTGATGGAGA	AACTTCCCAG	360
TGGCATGGAA	ATTTCTTTTG	CCCCTGCCAC	GTCCCATGAG	GCCCCAGCCA	TGATGGATAG	420
TCACATCAGC	AGCAGTGATG	CTGCTACCGA	GATGCTCAGC	CAGCCCAACC	ACCCAGCGG	480
CGAAGTCAAG	GCTGAAAATA	ACATTGAGAT	GGTGGGCGAG	TCCCAGGCGG	CCAAGGTCAT	540
TGTCTCTGTC	GAAGATGCTG	TGCCTACCAT	ATTCTGTGGC	AAGATCAAAG	GCCTCTCAGG	600
GGTGTCCACC	AAAAACTTCT	CCTTCAAAAG	AGAAGACTCC	GTGCTTCAGG	GCTATGACAT	660
CAACAGCCAA	GGGGAAGAGT	CCATGGGAAA	TGCAGAGCCC	CTTAGGAAAC	CCATCAAAAA	720
CCGGAGCATA	AAGTTAAAGA	AAGTGAATC	CCAGGAAGTA	CACATGCTCC	CAATCAAAAA	780
ACAACGGCTG	GCCACCTTTT	TTCCAAGAAA	GTAAATAACG	GCTTTTAAAA	ATTTGTATGA	840
TTATAATATG	GGGAAAGGTG	CATTGGTTTT	ATAAAAAGGC	ATTTAAAAACA	AATTATCTTT	900
GTTAATTATT	TTGGGGAGTA	GTTGGGAAAT	GGAAAGGTGA	ATTGGCTCTA	GAGGCCCTGT	960
ATGCTAGTAT	CATTTTCTTT	TTTAATTTTT	GACTTTTCAC	AAATGAGTAA	ATAAGAGCAA	1020
CCTATTTTTT	AAGCAGATTG	CACATTTTTT	GCAGCTTTAA	TGGAATATTG	GGTGAATTAG	1080
AGGGGTAAAA	AAAGCTATTT	TCATTGCCAC	AAAGTGCTTT	GATGATGTAA	TACCTAATAA	1140
AGGGTAGGAT	GAATATTTCA	CAATAAATGT	TTGTTTGCAC	TAAAAAATAA	AAAAAATAA	1200
AAAAAATAA	AAATTCCTGC	GGCCGC				1226

## (2) INFORMATION FOR SEQ ID NO:10:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1049 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GAATTCGGCA	CGAGGGCGCC	ATGGTGAAGG	TGACGTTCAA	CTCCGCTCTG	GCCCAGAAGG	60
AGGCCAAGAA	GGACGAGCCC	AAGAGCGGCG	AGGAGGCGCT	CATCATCCCC	CCCGACGCCG	120
TCGCGGTGGA	CTGCAAGGAC	CCAGATGATG	TGGTACCAGT	TGGCCAAAGA	AGAGCCTGGT	180
GTTGGTGCA	TGCTTTTGA	CTAGCATTTA	TGCTTGCAGG	TGTTATTCTA	GGAGGAGCAT	240
ACTTGTAACA	ATATTTTGCA	CTTCAACCAG	ATGACGTGTA	CTACTGTGGA	ATAAAGTACA	300
TCAAAGATGA	TGTCATCTTA	AATGAGCCCT	CTGCAGATGC	CCCAGCTGCT	CTCTACCAGA	360
CAATTGAAGA	AAATATTTAA	ATCTTTGAAG	AAGAAGAAGT	TGAATTTATC	AGTGTGCCTG	420
TCCCAGAGTT	TGCAGATAGT	GATCCTGCCA	ACATTGTTCA	TGACTTTAAC	AAGAACTTA	480
CAGCCTATTT	AGATCTTAAC	CTGGATAAGT	GCTATGTGAT	CCCTCTGAAC	ACTTCCATTG	540
TTATGCCACC	CAGAAACCTA	CTGGAGTTAC	TTATTAACAT	CAAGGCTGGA	ACCTATTTGC	600
CTCAGTCCTA	TCTGATTCAT	GAGCACATGG	TTATTACTGA	TCGCATTGAA	AACATTGATC	660
ACCTGGGTTT	CTTTATTTAT	CGACTGTGTC	ATGACAAGGA	AACTTACAAA	CTGCAACGCA	720
GAGAAACTAT	TAAAGGTATT	CAGAAACGTG	AAGCCAGCAA	TGTTTCGCA	ATTCGGCATT	780
TTGAAAACAA	ATTTGCCGTG	GAAACTTTAA	TTTGTTCTTG	AACAGTCAAG	AAAAACATTA	840
TTGAGGAAAA	TTAATATCAC	AGCATAACCC	CACCCTTTAC	ATTTTGTTGC	AGTTGATTAT	900
TTTTTAAAGT	CTTCTTTCAT	GTAAGTAGCA	AACAGGGCTT	TACTATCTTT	TCATCTCATT	960
AATTCAATTA	AAACCATTAC	CTTAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	1020
AAAAAAAAAA	AAAAAATTCC	TGCGGCCGC				1049

## (2) INFORMATION FOR SEQ ID NO:11:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1142 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GAATTCGGCA	CGAGGGGAGA	ATACTTTTTT	CGATGCCTAC	TGGAGACTTT	GATTCGAAGC	60
CCAGTTGGGC	CGACCAGGTG	GAGGAGGAGG	GGGAGGACGA	CAAATGTGTC	ACCAGCGAGC	120
TCCTCAAGGG	GATCCCTCTG	GCCACAGGTG	ACACCAGCCC	AGAGCCAGAG	CTACTGCCGG	180
GAGCTCCACT	GCCGCCTCCC	AAGGAGGTCA	TCAACGGAAA	CATAAAGACA	GTGACAGAGT	240
ACAAGATAGA	TGAGGATGGC	AAGAAGTTCA	AGATTGTCCG	CACCTTCAGG	ATTGAGACCC	300
GGAAGGCTTC	AAAGGCTGTC	GCAAGGAGGA	AGAAGTGGAA	GAAGTTCGGG	AACTCAGAGT	360
TTGACCCCCC	CGGACCCAAT	GTGGCCACCA	CCACTGTCAG	TGACGATGTC	TCTATGACGT	420
TCATCACCAG	CAAAGAGGAC	CTGAAGTGCC	AGGAGGAGGA	GGACCCTATG	AACAAATTCA	480
AGGGCCAGAA	GATCGTGTCC	TGCCGCATCT	GCAAGGGCGA	CCACTGGACC	ACCCGCTGCC	540
CCTACAAGGA	TACGCTGGGG	CCCATGCAGA	AGGAGCTGGC	CGAGCAGCTG	GGCCTGTCTA	600
CTGGCGAGAA	GGAGAAGCTG	CCGGGAGAGC	TAGAGCCGGT	GCAGGCCACG	CAGAACAAGA	660
CAGGGGAAGTA	TGTGCCGCCG	AGCCTGCGCG	ACGGGGCCAG	CCGCCGCGGG	GAGTCCATGC	720
AGCCCAACCG	CAGAGCCGAC	GACAACGCCA	CCATCCGTGT	CACCAACTTG	CGCAGAGGAC	780
ACGCGTGAGA	CCGACCTGCA	GGAGCTCTTC	CGGCCTTTTC	GCTCCATCTC	CCGCATCTAC	840
CTGGCTAAGG	ACAAGACCAC	TGGCCAATCC	AAGGGCTTTG	CCTTCATCAG	CTTCCACCGC	900



CGCGAGGATG	CTGCGCGTGC	CATTGCCGGG	GTGTCCGGCT	TTGGCTACGA	CCACCTCATC	960
CTCAACGTCG	AGTGGGCCAA	GCCGTCCACC	AACTAAGCCA	GCTGCCACTG	TGTACTCGGT	1020
CCGGGACCCCT	TGGCGACAGA	AGACAGCCTC	CGAGAGCGCG	GGCTCCAAGG	GCAATAAAGC	1080
AGCTCCACTC	TCAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAT	TCCTGCGGCC	1140
GC						1142

## (2) INFORMATION FOR SEQ ID NO:12:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1696 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GAATTCGGCA	CGAGGGAAAC	ATGGCGGTAG	GCTGGGACCA	TAACACAAGC	ATGACTATAT	60
GAAGGAAGAG	GAAGGTTTT	CTGAAGATGA	GGCGACTGAA	TCGGAAAAAA	ACTTTAAGTT	120
TGGTAAAGA	GTTGGATGCC	TTTCCGAAGG	TTCTGAGAG	CTATGTAGAG	ACTTCAGCCA	180
GTGGAGGTAC	AGTTTCTCTA	ATAGCATTTA	CAACTATGGC	TTTATTAACC	ATAATGGAAT	240
TCTCAGTATA	TCAAGATACA	TGGATGAAGT	ATGAATACGA	AGTAGACAAG	GATTTTTCTA	300
GCAAATTAAG	AATTAATATA	GATATTACTG	TTGCCATGAA	GTGTCAATAT	GTTGGAGCGG	360
ATGTATTGGA	TTTAGCAGAA	ACAATGGTTG	CATCTGCAGA	TGGTTTAGTT	TATGAACCAA	420
CAGTATTTGA	TCTTTCACCA	CAGCAGAAAG	AGTGGCAGAG	GATGCTGCAG	CTGATTCAGA	480
GTAGGCTACA	AGAAGAGCAT	TCACCTCAAG	ATGTGATATT	TAAAAGTGCT	TTTAAAAGTA	540
CATCAACAGC	TCTTCCACCA	AGAGAAGATG	ATTCATCACA	GTCTCCAAAT	GCATGCAGAA	600
TTCATGGCCA	TCTATATGTC	AATAAAGTAG	CAGGGAATTT	TCACATAACA	GTGGGCAAGG	660
CAATTCACA	TCCTCGTGGT	CATGCACATT	TGGCAGCACT	TGTCAACCAT	GAATCTTACA	720
ATTTTTCTCA	TAGAATAGAT	CATTTGTCTT	TTGGAGAGCT	TGTTCCAGCA	ATTATTAATC	780
CTTTAGATGG	AACTGAAAAA	ATTGCTATAG	ATCACAACCA	GATGTTCCAA	TATTTTATTA	840
CAGTTGTGCC	AACAAAACCTA	CATACATATA	AAATATCAGC	AGACACCCAT	CAGTTTTCTG	900
TGACAGAAAG	GGAACGTATC	ATTAACCATG	CTGCAGGCAG	CCATGGAGTC	TCTGGGATAT	960
TTATGAAATA	TGATCTCAGT	TCTCTTATGG	TGACAGTTAC	TGAGGAGCAC	ATGCCATTCT	1020
GGCAGTTTTT	TGTAAGACTC	TGTGGTATTG	TTGGAGGAAT	CTTTTCAACA	ACAGGCATGT	1080
TACATGGAAT	TGGAAAATTT	ATAGTTGAAA	TAATTTGCTG	TCGTTTCAGA	CTTGGATCCT	1140
ATAAACCTGT	CAATTCTGTT	CCTTTTGAGG	ATGGCCACAC	AGACAACCAC	TTACCTCTTT	1200
TAGAAAATAA	TACACATTAA	CACCTCCCGA	TTGAAGGAGA	AAAACTTTTT	GCCTGAGACA	1260
TAAAACCTTT	TTTAAATAAT	AAAATATTGT	GCAATATATT	CAAAGAAAAA	AAAACACAAA	1320
TAAGCAGAAA	ACATACTTAT	TTTAAAAAAG	AAAAAAAAGG	ATAAAAAAAC	CCAAACTGAA	1380
ATTCTATATA	CGTTGTGTCT	GTTACAAATG	TCGTAGAAGA	AATCATGCAG	CTAAACGATG	1440
AAGAAGCCCA	ACTGGAGTGT	TGCTTTGAAG	ATGACGCCTT	CTTATATTTT	CATAGCAAAT	1500
GGGTGGTATC	AAAATCAGAC	ATTGCTTCTT	GCTGATAAAA	AGCCTGAAGG	AAATAAGTGA	1560
AACTACATCT	ATGGGAAAAA	AAAAAACATT	GAGAAGTGCA	AATGTTTCGA	TCCTTTTGTT	1620
TTTAAAAGAT	ATGATGTCAG	AATAAAATGT	GGAAAACATA	CGGAAAAAAA	AAAAAAAATA	1680
AAATTCCTGC	GGCCGC					1696

## (2) INFORMATION FOR SEQ ID NO:13:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1100 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GAATTCGGCA	CGAGGCGGCA	CGAGGCGGCA	CGAGGGTGGC	ATATCACGGC	CATGGGGTCT	60
CAGCATTCGG	CTGCTGCTCG	CCCCTCCTCC	TGCAGGCGAA	AGCAAGAAGA	TGACAGGGAC	120
GGTTTGCTGG	CTGAACGAGA	GCAGGAAGAA	GCCATTGCTC	AGTTCCCAT	TGTGGAATTC	180
ACCGGGAGAG	ATAGCATCAC	CTGTCTCACG	TGCCAGGGGA	CAGGCTACAT	TCCAACAGAG	240
CAAGTAAATG	AGTTGGTGGC	TTTGATCCCA	CACAGTGATC	AGAGATTGCG	CCCTCAGCGA	300
ACTAAGCAAT	ATGTCTCCT	GTCCATCCTG	CTTTGTCTCC	TGGCATCTGG	TTTGGTGGTT	360
TTCTTCCTGT	TTCCGCATTC	AGTCCTTGTG	GATGATGACG	GCATCAAAGT	GGTGAAAGTC	420
ACATTTAATA	AGCAAGACTC	CCTTGTAATT	CTCACCATCA	TGGCCACCCT	GAAAATCAGG	480
AACTCCAAC	TCTACACGGT	GGCAGTGACC	AGCCTGTCCA	GCCAGATTCA	GTACATGAAC	540
ACAGTGGTCA	GTACATATGT	GACTACTAAC	GTCTCCCTTA	TTCCACCTCG	GAGTGAGCAA	600
CTGGTGAATT	TTACCGGGAA	GGCCGAGATG	GGAGGACCGT	TTTCCTATGT	GTACTTCTTC	660
TGCACGGTAC	CTGAGATCCT	GGTGCAACAAC	ATAGTGATCT	TCATGCGAAC	TTCAGTGAAG	720
ATTTCATACA	TTGGCCTCAT	GACCCAGAGC	TCCTTGGAGA	CACATCACTA	TGTGGATTGT	780
GGAGGAAATT	CCACAGCTAT	TTAACAAC	CTATTGGTTC	TTCCACACAG	CGCCTGTAGA	840
AGAGAGCACA	GCATATGTTT	CCAAGGCCTG	AGTTCTGGAC	CTACCCCCAC	GTGGTGTAAAG	900
CAGAGGAGGA	ATTGGTTCAC	TTAACTCCCA	GCAAACATCC	TCCTGCCACT	TAGGAGGAAA	960
CACCTCCCTA	TGGTACCATT	TATGTTTCTC	AGAACCAGCA	GAATCAGTGC	CTAGCCTGTG	1020
CCCAGCAAAT	AGTTGGCACT	CAATAAAGAT	TTGCAGAATT	TAAAAA	AAAAA	1080
AAAAAATTC	CTGCGGCCGC					1100

## (2) INFORMATION FOR SEQ ID NO:14:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1588 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GAATTCGGCA	CGAGGGTACC	TGCTTTTCTA	TTGCCTCTTT	GAAACAATGG	TCACGTGTTT	60
CCATGTTCCC	TACTCGGCTC	TCACCATGTT	CATCAGCACC	GAGCAGACTG	AGCGGGATTC	120
TGCCACCGCC	TATCGGATGA	CTGTGGAAGT	GCTGGGCACA	GTGCTGGGCA	CGCGGATCCA	180
GGGACAAATC	GTGGGCCAAG	CAGACACGCC	TTGTTTCCAG	GACCTCAATA	GCTCTACAGT	240
AGCTTCACAA	AGTGCCAACC	ATACACATGG	CACCACCTCA	CACAGGGAAA	CGCAAAAGGC	300
ATACCTGCTG	GCAGCGGGGG	TCATTGTCTG	TATCTATATA	ATCTGTGCTG	TCATCCTGAT	360
CCTGGGCGTG	CGGGAGCAGA	GAGAACCTTA	TGAAGCCAG	CAGTCTGAGC	CAATCGCCTA	420
CTTCCGGGGC	CTACGGCTGG	TCATGAGCCA	CGGCCCATAC	ATCAAACCTTA	TTACTGGCTT	480
CCTCTTCACC	TCCTTGCTT	TCATGCTGGT	GGAGGGGAAC	TTTGTCTTGT	TTTGCACCTA	540
CACCTTGGGC	TTCCGCAATG	AATTCCAGAA	TCTACTCCTG	GCCATCATGC	TCTCGGCCAC	600
TTTAACCATT	CCCATCTGGC	AGTGGTTCTT	GACCCGGTTT	GGCAAGAAGA	CAGCTGTATA	660
TGTTGGGATC	TCATCAGCAG	TGCCATTTCT	CATCTTGGTG	GCCCTCATGG	AGAGTAACCT	720
CATCATTACA	TATGCGGTAG	CTGTGGCAGC	TGGCATCAGT	GTGGCAGCTG	CCTTCTTACT	780
ACCCTGGTCC	ATGCTGCCTG	ATGTCATTGA	CGACTTCCAT	CTGAAGCAGC	CCCACTTCCA	840
TGGAACCGAG	CCCATCTTCT	TCTCCTTCTA	TGTCTTCTTC	ACCAAGTTTG	CCTCTGGAGT	900
GTCAGTGGGC	ATTTCTACCC	TCAGTCTGGA	CTTTGCAGGG	TACCAGACCC	GTGGCTGCTC	960
GCAGCCGGAA	CGTGTCAAGT	TTACACTGAA	CATGCTCGTG	ACCATGGCTC	CCATAGTTCT	1020
CATCCTGCTG	GGCCTGCTGC	TCTTCAAAAT	GTACCCCAT	GATGAGGAGA	GGCGGCGGCA	1080
GAATAAGAAG	GCCCTGCAGG	CACTGAGGGA	CGAGGCCAGC	AGCTCTGGCT	GCTCAGAAAC	1140
AGACTCCACA	GAGCTGGCTA	GCATCCTCTA	GGGCCCGCCA	CGTTGCCCGA	AGCCACCATG	1200
CAGAAGGCCA	CAGAAGGAT	CAGGACCTGT	TGCGCGGCTT	GCTGAGCAGC	TGGACTGCAG	1260
GTGCTAGGAA	GGGAAGTGAA	GACTCAAGGA	GGTGGCCAG	GACACTTGCT	GTGCTCACTG	1320
TGGGGCCGGC	TGCTCTGTGG	CCTCCTGCCT	CCCCTCTGCC	TGCCTGTGGG	GCCAAGCCCT	1380
GGGCTGCCA	CTGTGAATAT	GCCAAGGACT	GATCGGGCCT	AGCCCGGAAC	ACTAATGTAG	1440
AAACCTTTTT	TTTACAGAGC	CTAATTAATA	ACTTAATGAC	TGTGTACATA	GCAATGTGTG	1500

TGTATGTATA TGTCTGTGAG CTATTAATGT TATTAATTTT CATAAAAGCT GGAAAGCAAA 1560  
 AAAAAAAAAA AAAAATTCCT GCGGCCGC 1588

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1535 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GAATTCGGCA CGAGGCGGAA GTCCCGTCTC ACGGTTGCCC TGGCAGCGCG CGAGGCTGGT 60  
 GAGTCGGCAG CCCTGTGGCA GCCGGCGGGC TGGTTTCCAT GGTTGCACGA TTAGGAACCA 120  
 CCAGCTGCTG CATCCCATGG CCAGGGGTGG CGTCCAGGTG GCAGAGCAGC TAGGAACGCA 180  
 AGGCCTGAAC CTGGGGCCAG ACACCTTGCT CTCCCGGCCA TGGTCAACGA CCCTCCAGTA 240  
 CCTGCCTTAC TGTGGGCCCA GGAGGTGGGC CAAGTCTTGG CAGGCCGTGC CCGCAGGCTG 300  
 CTGCTGCAGT TTGGGGTGCT CTTCTGCACC ATCCTCCTTT TGCTCTGGGT GTCTGTCTTC 360  
 CTCTATGGCT CCTTCTACTA TTCCTATATG CCGACAGTCA GCCACCTCAG CCCTGTGCAT 420  
 TTCTACTACA GGACCGACTG TGATTCCCTC ACCACCTCAC TCTGTCCTT CCCTGTTGCC 480  
 AATGTCTCGC TGAATAAGGG TGGACGTGAT CGGGTGCTGA TGTATGGACA GCCGTATCGT 540  
 GTTACCTTAG AGCTTGAGCT GCCAGAGTCC CCTGTGAATC AAGATTTGGG CATGTTCTTG 600  
 GTCACCATT CTGCTACAC CAGAGGTGGC CGAATCATCT CCACTTCTTC GCGTTCGGTG 660  
 ATGCTGCATT ACCGCTCAGA CCTGCTCCAG ATGCTGGACA CACTGGTCTT CTCTAGCCTC 720  
 CTGCTATTTG GCTTTGCAGA GCAGAAGCAG CTGCTGGAGG TGGAACCTCTA CGCAGACTAT 780  
 AGAGAGAACT CGTACGTGCC GACCACTGGA GCGATCATTG AGATCCACAG CAAGCGCATC 840  
 CAGCTGTATG GAGCCTACCT CCGCATCCAC GCGCACTTCA CTGGGCTCAG ATACCTGCTA 900  
 TACAACTTCC CGATGACCTG CGCCTTCATA GGTGTTGCCA GCAACTTCAC CTTCTCAGC 960  
 GTCATCGTGC TCTTCAGCTA CATGCAGTGG GTGTGGGGGG GCATCTGGCC CCGACACCGC 1020  
 TTCTCTTTGC AGGTTAACAT CCGAAAAAGA GACAATTCCC GGAAGGAAGT CCAACGAAGG 1080  
 ATCTCTGCTC ATCAGCCAGG GCCTGAAGGC CAGGAGGAGT CAACTCCGCA ATCAGATGTT 1140  
 ACAGAGGATG GTGAGAGCCC TGAAGATCCC TCAGGGACAG AGGTCAGCTG TCCGAGGAGG 1200  
 AGAAACCAGA TCAGCAGCCC CTGAGCGGAG AAGAGGAGCT AGAGCCTGAG GCCAGTGATG 1260  
 GTTCAGGCTC CTGGGAAGAT GCAGCTTTGC TGACGGAGGC CAACCTGCCT GCTCCTGCTC 1320  
 CTGCTTCTGC TTCTGCCCTT GTCCTAGAGA CTCTGGGCAG CTCTGAACCT GCTGGGGGTG 1380  
 CTCTCCGACA GCGCCCCACC TGCTCTAGTT CCTGAAGAAA AGGGGCAGAC TCCTCACATT 1440  
 CCAGCACTTT CCCACCTGAC TCCTCTCCCC TCGTTTTTCC TTCAATAAAC TATTTTGTGT 1500  
 CAAAAAAAAA AAAAAAAAAA AATTCCTGCG GCCGC 1535

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1322 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GAATTCGGCA CGAGGGCGGG CGCTACGGGC TTGACTCCCC CAAGGCCGAG GTCCGCGGCC 60  
 AGGTGCTGGC GCCGCTGCCC CTCCACGGAG TTGCTGATCA TCTGGGCTGT GATCCACAAA 120  
 CCCGGTTCTT TGTCCCTCCT AATATCAAAC AGTGGATTGC CTTGCTGCAG AGGGGAAACT 180  
 GCACGTTTAA AGAGAAAATA TCACGGGCCG CTTTCCACAA TGCAATTGCT GTAGTCATCT 240  
 ACAATAATAA ATCCAAAGAG GAGCCAGTTA CCATGACTCA TCCAGGCACT GGAGATATTA 300

TTGCTGTCAT	GATAACAGAA	TTGAGGGGTA	AGGATATTTT	GAGTTATCTG	GAGAAAAACA	360
TCTCTGTACA	AATGACAATA	GCTGTTGGAA	CTCGAATGCC	ACCGAAGAAC	TTCAGCCGTG	420
GCTCTCTAGT	CTTCGTGTCA	ATATCCTTTA	TTGTTTTGAT	GATTATTTCT	TCAGCATGGC	480
TCATATTCTA	CTTCATTCAA	AAGATCAGGT	ACACAAATGC	ACGCGACAGG	AACCAGCGTC	540
GTCTCGGAGA	TGCAGCCAAG	AAAGCCATCA	GTAAATTGAC	AACCAGGACA	GTAAGAAGG	600
GTGACAAGGA	AACTGACCCA	GACTTTGATC	ATTGTGCAGT	CTGCATAGAG	AGCTATAAGC	660
AGAATGATGT	CGTCCGAATT	CTCCCCTGCA	AGCATGTTTT	CCACAAATCC	TGCGTGATC	720
CCTGGCTTAG	TGAACATTGT	ACCTGTCCTA	TGTGCAAAC	TAATATATTG	AAGGCCCTGG	780
GAATTGTGCC	GAATTTGCCA	TGTACTGATA	ACGTAGCATT	CGATATGGAA	AGGCTCACCA	840
GAACCAAGC	TGTAAACCGA	AGATCAGCCC	TCGGCGACCT	CGCCGGCGAC	AACTCCCTTG	900
GCCTTGAGCC	ACTTCGAACT	TCGGGGATCT	CACCTCTTCC	TCAGGATGGG	GAGCTCACTC	960
CGAGAACAGG	AGAAATCAAC	ATTGCAGTAA	CAAAAGAATG	GTTTATTATT	GCCAGTTTTG	1020
GCCTCCTCAG	TGCCCTCACA	CTCTGCTACA	TGATCATCAG	AGCCACAGCT	AGCTTGAATG	1080
CTAATGAGGT	AGAATGGTTT	TGAAGAAGAA	AAAACCTGCT	TTCTGACTGA	TTTTGCCTTG	1140
AAGGAAAAAA	GAACCTATTT	TTGTGCATCA	TTTACCAATC	ATGCCACACA	AGCATTTATT	1200
TTTAGTACAT	TTTATTTTTT	CATAAAATTG	CTAATGCCAA	AGCTTTGTAT	TAAAAGAAAT	1260
AAATAATAAA	ATAAAAAAAA	AAAAAATAAA	AAAAAATAAA	AAAAAATAAT	TCCTGCGGCC	1320
GC						1322

## (2) INFORMATION FOR SEQ ID NO:17:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1711 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GAATTCGGCA	CGAGGCCCTC	CCGCGCTCCC	GGGCGCGCG	GGCCGCGCCC	CCGACGCCCT	60
ACATATACTC	AGGTGCGCCC	CACCTGTCCG	CCCGCACCTG	CTGGCTCACC	TCCGAGCCAC	120
CTCTGCTGCG	CACCGCAGCC	TCGGACCTAC	AGCCCAGGAT	ACTTTGGGAC	TTGCCGGCGC	180
TCAGAAACGC	GCCCAGACGG	CCCTCCACC	TTTTGTTTGC	CTAGGGTCGC	CGAGAGCGCC	240
CGGAGGGAAC	CGCCTGGCCT	TCGGGGACCA	CCAATTTTGT	CTGGAACCAC	CCTCCCGGCG	300
TATCCTACTC	CCTGTGCCGC	GAGGCCATCG	CTTCACTGGA	GGGGTCGATT	TGTGTGTAGT	360
TTGGTGACAA	GATTTGCATT	CACCTGGCCC	AAACCCTTTT	TGTCTCTTTG	GGTGACCGGA	420
AAACTCCACC	TCAAGTTTTT	TTTTGTGGGG	CTGCCCCCA	AGTGTCGTTT	GTTTTACTGT	480
AGGGTCTCCC	GCCCGGCGCC	CCAGTGTTT	TCTGAGGGCG	GAAATGGCCA	ATTCGGGCCT	540
GCAGTTGCTG	GGCTTCTCCA	TGGCCCTGCT	GGGCTGGGTG	GGTCTGGTGG	CCTGCACCGC	600
CATCCCGCAG	TGGCAGATGA	GCTCCTATGC	GGGTGACAAC	ATCATCACGG	CCCAGGCCAT	660
GTACAAGGGG	CTGTGGATGG	ACTGCGTCAC	GCAGAGCACG	GGGATGATGA	GCTGCAAAAT	720
GTACGACTCG	GTGCTCGCCC	TGTCCGCGGC	CTTGCAGGCC	ACTCGAGCCC	TAATGGTGGT	780
CTCCCTGGTG	CTGGGCTTCC	TGGCCATGTT	TGTGGCCACG	ATGGGCATGA	AGTGCACGCG	840
CTGTGGGGGA	GACGACAAAG	TGAAGAAGGC	CCGTATAGCC	ATGGGTGGAG	GCATAATTTT	900
CATCGTGGCA	GGTCTTGCCG	CCTTGGTAGC	TTGCTCCTGG	TATGGCCATC	AGATTGTCAC	960
AGACTTTTAT	AACCCTTTGA	TCCCTACCAA	CATTAAGTAT	GAGTTTGGCC	CTGCCATCTT	1020
TATTGGCTGG	GCAGGTCTG	CCCTAGTCAT	CCTGGGAGGT	GCACTGCTCT	CCTGTTCCCTG	1080
TCCTGGGAAT	GAGAGCAAGG	CTGGGTACCG	TGCACCCCGC	TCTTACCCTA	AGTCCAACCTC	1140
TTCCAAGGAG	TATGTGTGAC	CTGGGATCTC	CTTGCCCCAG	CCTGACAGGC	TATGGGAGTG	1200
TCTAGATGCC	TGAAAGGGCC	TGGGGCTGAG	CTCAGCCTGT	GGGCAGGGTG	CCGGACAAAG	1260
GCCTCCTGGT	CACCTGTCTC	CTGACTCCA	TGTATAGTCC	TCTTGGGTTG	GGGGTGGGGG	1320
GGTGCCGTTG	GTGGGAGAGA	CAAAAAGAGG	GAGAGTGTGC	TTTTTGTACA	GTAATAAAAA	1380
ATAAGTATTG	GGAAGCAGGC	TTTTTTCCCT	TCAGGGCCTC	TGCTTTCCTC	CCGTCCAGAT	1440
CCTTGCAGGG	AGCTTGGAAC	CTTAGTGCAC	CTACTTCAGT	TCAGAACACT	TAGCACCCCA	1500
CTGACTCCAC	TGACAATTGA	CTAAAAGATG	CAGGTGCTCG	TATCTCGACA	TTCATTCCCA	1560
CCCCCTCTT	ATTTAAATAG	CTACCAAGT	ACTTCTTTTT	TAATAAAAA	ATAAAGATTT	1620

TTATTAGGTA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1680  
 AAAAAAAAAA AAAAAAATT CCTGCGGCCG C 1711

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1553 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GAATTCGGCA CGAGGGCAGG TCCAGAGTAA AGTCACTGAA GAGTGGGAAGC GAGGAAGGAA 60  
 CAGGATGATT AGACCTCAGC TGCGGACCGC GGGGCTGGGA CGATGCCTCC TGCCGGGGCT 120  
 GCTGCTGCTC CTGGTGCCCG TCCTCTGGGC CGGGGCTGAA AAGCTACATA CCCAGCCCTC 180  
 CTGCCCCGCG GTCTGCCAGC CCACGCGCTG CCCGCGCTG CCCACCTGCG CGCTGGGGAC 240  
 CACGCCGGTG TTCGACCTGT GCCGCTGTTG CCGCGTCTGC CCCGCGGCCG AGCGTGAAGT 300  
 CTGCGGCGGG GCGCAGGGCC AACCCTGCGC CCCGGGGCTG CAGTGCCTCC AGCCGCTGCG 360  
 CCCCCGGTTC CCCAGCACCT GCGGTTGCCC GACGCTGGGA GGGGCCGTGT GCGGCAGCGA 420  
 CAGGCGCACC TACCCAGCA TGTGCGCGCT CCGGGCCGAA AACCGCGCCG CGCGCCGCCT 480  
 GGGCAAGGTC CCGGCCGTGC CTGTGCAGTG GGGGAAGTGC GGGGATACAG GGACCAGAAG 540  
 CGCAGGCCCG CTCAGGAGGA ATTACAATT CATCGCCGCG GTGGTGGAGA AGGTGGCGCC 600  
 ATCGGTGGTT CACGTGCAGC TGTGGGGCAG GTTACTTCAC GGCAGCAGGC TTGTTCCCTGT 660  
 GTACAGTGGC TCTGGGTTCA TAGTGTCTGA GGACGGGCTC ATTATTACCA ATGCCCATGT 720  
 TGTCAAGGAT ATTGACCTTA AATTGGATCT TGCGGTGATT AAGATTGAAT CAAATGCTGA 840  
 ACTTCCTGTA CTGATGCTGG GAAGATCATC TGACCTTCGG GCTGGAGAGT TTGTGGTGGC 900  
 TTTGGGCAGC CCATTTTCTC TGCAGAACAC AGTACTGCA GGAATTGTCA GCACCAAACA 960  
 GCGAGGGGGC AAAGAACTGG GGATGAAGGA TTCAGATATG GACTACGTCC AGATTGATGC 1020  
 CACAATTAAC TATGGGAATT CTGGTGGTCC TCTGGTGAAC TTGGATGGTG ATGTGATTGG 1080  
 CGTCAATTCA TTGAGGGTGA CTGATGGAAT CTCCTTTGCA ATTCCTTCAG ATCGAGTTAG 1140  
 GCAGTCTTGT GCAGAATACC ATGAGCACCA GATGAAAGGA AAGGCGTTTT CAAATAAGAA 1200  
 ATATCTGGGT CTGCAAATGC TGTCCCTCAC TGTGCCCTT AGTGAAGAAT TGAAAATGCA 1260  
 TTATCCAGAT TTCCCTGATG TGAGTCTGG GGTATATGTA TGTAAGTGG TTGAAGGAAC 1320  
 AGCTGCTCAA AGCTCTGGAT TGAGAGATCA CGATGTAATT GTCAACATAA ATGGGAAACC 1380  
 TATTACTACT ACAACTGATG TTGTTAAAGC TCTTGACAGT GATTCCCTTT CCATGGCTGT 1440  
 TCTTCGGGGA AAAGATAATT TGCTCTGAC AGTCATACCT GAAACAATCA ATTAAATATC 1500  
 TTGTTTTTAA GTGGGATTAT CTAAAAAAA AAAAAAAA TTCCTGCGGC CGC 1553

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1596 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GAATTCGGCA CGAGGGGAGC CGCTCCCGGA GCGCGGCCGT AGAGGCTGCA ATCGCAGCCG 60  
 GGAGCCCGCA GCGCGCGCCC CGAGCCCGCC GCGGCCCTTC GAGGGCGCCC CAGGCCGCGC 120  
 CATGGTGAAG GTGACGTTCA ACTCCGCTCT GGCCAGAAAG GAGGCCAAGA AGGACGAGCC 180  
 CGAGAGCGGC GAGGAGGCGC TCATCATCCC CCCCAGCGCC GTCGCGGTGG ACTGCAAGGA 240

```

CCCAGATGAT GTGGTACCAG TTGGCCAAAG AAGAGCCTGG TGTGGTGCA TGTGCTTTGG 300
ACTAGCATTT ATGCTTGACG GTGTTATTCT AGGAGGAGCA TACTTGTACA AATATTTTGC 360
ACTTCAACCA GATGACGTGT ACTACTGTGG AATAAAGTAC ATCAAAGATG ATGTCATCTT 420
AAATGAGCCC TCTGCAGATG CCCCAGCTGC TCTCTACCAG ACAATTGAAG AAAATATTAA 480
AATCTTTGAA GAAGAAGAAG TTGAATTTAT CAGTGTGCCT GTCCCAGAGT TTGCAGATAG 540
TGATCCTGCC AACATTGTTT ATGACTTTAA CAAGAAACTT ACAGCCTATT TAGATCTTAA 600
CCTGGATAAG TGCTATGTGA TCCCTCTGAA CACTTCCATT GTTATGCCAC CCAGAAACCT 660
ACTGGAGTTA CTTATTAACA TCAAGGCTGG AACCTATTTG CCTCAGTCCT ATCTGATTCA 720
TGAGCACATG GTTATTACTG ATCGCATTGA AAACATTGAT CACCTGGGTT TCTTTATTTA 780
TCGACTGTGT CATGACAAGG AAACCTACAA ACTGCAACGC AGAGAAACTA TTAAAGGTAT 840
TCAGAAACGT GAAGCCAGCA ATTGTTTCGC AATTCGGCAT TTTGAAAACA AATTTGCCGT 900
GGAAACTTTA ATTTGTTCTT GAACAGTCAA GAAAACATT ATTGAGGAAA ATTAATATCA 960
CAGCATAACC CCACCCTTTA CATTTTGTGC AGTGATATTT TTTAAAGTCT CTTTCATGTA 1020
AGTAGCAAAC AGGGCTTTAC TATCTTTTCA TCTCATTAAT TCAATTAAAA CCATTACCTT 1080
AAAATTTTTT TCTTTCGAAG TGTGGTGTCT TTTATATTTG AATTAGTAAC TGTATGAAGT 1140
CATAGATAAT AGTACATGTC ACCTTAGGTA GTAGGAAGAA TTACAATTTT TTTAAATCAT 1200
TTATCTGGAT TTTTATGTTT TATTAGCATT TTCAAGAAGA CGGATTATCT AGAGAATAAT 1260
CATATATATG CATACGTAAA AATGGACCAC AGTGACTTAT TTGTAGTTGT TAGTTGCCCT 1320
GCTACCTAGT TTGTTAGTGC ATTTGAGCAC ACATTTTAAAT TTTCTCTTAA TTAAATGTG 1380
CAGTATTTTC AGTGTCAAAT ATATTTAACT ATTTAGAGAA TGATTTCCAC CTTTATGTTT 1440
TAATATCCTA GGCATCTGCT GTAATAATAT TTTAGAAAAT GTTTGGAATT TAAGAAATAA 1500
CTTGTGTTAC TAATTTGTAT AACCCATATC TGTGCAATGG AATATAAATA TCACAAAGTT 1560
GTTTAAAAAA AAAAAAAAAA AAATTCCTGC GGCCGC 1596

```

## (2) INFORMATION FOR SEQ ID NO:20:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: None

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

```

Met Ala Trp Arg Arg Arg Glu Ala Gly Val Gly Ala Arg Gly Val Leu
 1           5           10           15
Ala Leu Ala Leu Leu Ala Leu Ala Leu Cys Val Pro Gly Ala Arg Gly
 20           25           30
Arg Ala Leu Glu Trp Phe Ser Ala Val Val Asn Ile Glu Tyr Val Asp
 35           40           45
Pro Gln Thr Asn Leu Thr Val Trp Ser Val Ser Glu Ser Gly Arg Phe
 50           55           60
Gly Asp Ser Ser Pro Lys Glu Gly Ala His Gly Leu Val Gly Val Pro
 65           70           75           80
Trp Ala Pro Gly Gly Asp Leu Glu Gly Cys Ala Pro Asp Thr Arg Phe
 85           90           95
Phe Val Pro Glu Pro Gly Gly Arg Gly Ala Ala Pro Trp Val Ala Leu
100           105           110
Val Ala Arg Gly Gly Cys Thr Phe Lys Asp Lys Val Leu Val Ala Ala
115           120           125
Arg Arg Asn Ala Ser Ala Val Val Leu Tyr Asn Glu Glu Arg Tyr Gly
130           135           140
Asn Ile Thr Leu Pro Met Ser His Ala Gly Thr Gly Asn Ile Val Val
145           150           155           160
Ile Met Ile Ser Tyr Pro Lys Gly Arg Glu Ile Leu Glu Leu Val Gln

```

```

          165          170          175
Lys Gly Ile Pro Val Thr Met Thr Ile Gly Val Gly Thr Arg His Val
          180          185          190
Gln Glu Phe Ile Ser Gly Gln Ser Val Val Phe Val Ala Ile Ala Phe
          195          200          205
Ile Thr Met Met Ile Ile Ser Leu Ala Trp Leu Ile Phe Tyr Tyr Ile
          210          215          220
Gln Arg Phe Leu Tyr Thr Gly Ser Gln Ile Gly Ser Gln Ser His Arg
          225          230          235          240
Lys Glu Thr Lys Lys Val Ile Gly Gln Leu Leu Leu His Thr Val Lys
          245          250          255
His Gly Glu Lys Gly Ile Asp Val Asp Ala Glu Asn Cys Ala Val Cys
          260          265          270
Ile Glu Asn Phe Lys Val Lys Asp Ile Ile Arg Ile Leu Pro Cys Lys
          275          280          285
His Ile Phe His Arg Ile Cys Ile Asp Pro Trp Leu Leu Asp His Arg
          290          295          300
Thr Cys Pro Met Cys Lys Leu Asp Val Ile Lys Ala Leu Gly Tyr Trp
          305          310          315          320
Gly Glu Pro Gly Asp Val Gln Glu Met Pro Ala Pro Glu Ser Pro Pro
          325          330          335
Gly Arg Asp Pro Ala Ala Asn Leu Ser Leu Ala Leu Pro Asp Asp Asp
          340          345          350
Gly Ser Asp Asp Ser Ser Pro Pro Ser Ala Ser Pro Ala Glu Ser Glu
          355          360          365
Pro Gln Cys Asp Pro Ser Phe Lys Gly Asp Ala Gly Glu Asn Thr Ala
          370          375          380
Leu Leu Glu Ala Gly Arg Ser Asp Ser Arg His Gly Gly Pro Ile Ser
          385          390          395          400

```

## (2) INFORMATION FOR SEQ ID NO:21:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: None

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

```

Met Asp Lys Gly Ser Ala Gly His Pro Gly Gly Val Leu Val Trp Gly
 1          5          10          15
Arg Ser Pro Ala Pro Thr Ala Leu Trp Gly Ala Ser Pro Trp Leu Ser
          20          25          30
Pro Leu Thr Ser Ala Leu Arg Gln Pro Leu His Arg Ala Pro Leu Leu
          35          40          45
Pro Gly Gln Leu Cys Trp Ser Pro Arg Pro Leu Glu Lys Asn Lys Ala
          50          55          60
Met Gly Arg Pro Leu Leu Pro Leu Leu Leu Leu Gln Pro Pro
          65          70          75          80
Ala Phe Leu Gln Pro Gly Gly Ser Thr Gly Ser Gly Pro Ser Tyr Leu
          85          90          95
Tyr Gly Val Thr Gln Pro Lys His Leu Ser Ala Ser Met Gly Gly Ser
          100          105          110
Val Glu Ile Pro Phe Ser Phe Tyr Tyr Pro Trp Glu Leu Ala Ile Val

```

```

      115      120      125
Pro Asn Val Arg Ile Ser Trp Arg Arg Gly His Phe His Gly Gln Ser
  130      135      140
Phe Tyr Ser Thr Arg Pro Ser Ile His Lys Asp Tyr Val Asn Arg
  145      150      155      160
Leu Phe Leu Asn Trp Thr Glu Gly Gln Glu Ser Gly Phe Leu Arg Ile
      165      170      175
Ser Asn Leu Arg Lys Glu Asp Gln Ser Val Tyr Phe Cys Arg Val Glu
      180      185      190
Leu Asp Thr Arg Arg Ser Gly Arg Gln Gln Leu Gln Ser Ile Lys Gly
      195      200      205
Thr Lys Leu Thr Ile Thr Gln Ala Val Thr Thr Thr Thr Thr Trp Arg
  210      215      220
Pro Ser Ser Thr Thr Thr Ile Ala Gly Leu Arg Val Thr Glu Ser Lys
  225      230      235      240
Gly His Ser Glu Ser Trp His Leu Ser Leu Asp Thr Ala Ile Arg Val
      245      250      255
Ala Leu Ala Val Ala Val Leu Lys Thr Val Ile Leu Gly Leu Leu Cys
      260      265      270
Leu Leu Leu Leu Trp Trp Arg Arg Arg Lys Gly Ser Arg Ala Pro Ser
      275      280      285
Ser Asp Phe
  290

```

## (2) INFORMATION FOR SEQ ID NO:22:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: None

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

```

Met Thr Val Ser Gln Arg Phe Gln Leu Ser Asn Ser Gly Pro Asn Ser
  1      5      10      15
Thr Ile Lys Met Lys Ile Ala Leu Arg Val Leu His Leu Glu Lys Arg
      20      25      30
Glu Arg Pro Asp His Gln His Ser Ala Gln Val Lys Arg Pro Ser
      35      40      45
Val Ser Lys Glu Gly Arg Lys Thr Ser Ile Lys Ser His Met Ser Gly
      50      55      60
Ser Pro Gly Pro Gly Gly Ser Asn Thr Ala Pro Ser Thr Pro Val Ile
      65      70      75      80
Gly Gly Ser Asp Lys Pro Gly Met Glu Glu Lys Ala Gln Pro Pro Glu
      85      90      95
Ala Gly Pro Gln Gly Leu His Asp Leu Gly Arg Ser Ser Ser Ser Leu
      100      105      110
Leu Ala Ser Pro Gly His Ile Ser Val Lys Glu Pro Thr Pro Ser Ile
      115      120      125
Ala Ser Asp Ile Ser Leu Pro Ile Ala Thr Gln Glu Leu Arg Gln Arg
      130      135      140
Leu Arg Gln Leu Glu Asn Gly Thr Thr Leu Gly Gln Ser Pro Leu Gly
      145      150      155      160
Gln Ile Gln Leu Thr Ile Arg His Ser Ser Gln Arg Asn Lys Leu Ile

```

1  
2  
3  
4  
5  
6  
7  
8  
9  
10  
11  
12  
13  
14  
15  
16  
17  
18  
19  
20  
21  
22  
23  
24  
25  
26  
27  
28  
29  
30  
31  
32  
33  
34  
35  
36  
37  
38  
39  
40  
41  
42  
43  
44  
45  
46  
47  
48  
49  
50  
51  
52  
53  
54  
55  
56  
57  
58  
59  
60  
61  
62  
63  
64  
65  
66  
67  
68  
69  
70  
71  
72  
73  
74  
75  
76  
77  
78  
79  
80  
81  
82  
83  
84  
85  
86  
87  
88  
89  
90  
91  
92  
93  
94  
95  
96  
97  
98  
99  
100  
101  
102  
103  
104  
105  
106  
107  
108  
109  
110  
111  
112  
113  
114  
115  
116  
117  
118  
119  
120  
121  
122  
123  
124  
125  
126  
127  
128  
129  
130  
131  
132  
133  
134  
135  
136  
137  
138  
139  
140  
141  
142  
143  
144  
145  
146  
147  
148  
149  
150  
151  
152  
153  
154  
155  
156  
157  
158  
159  
160  
161  
162  
163  
164  
165  
166  
167  
168  
169  
170  
171  
172  
173  
174  
175  
176  
177  
178  
179  
180  
181  
182  
183  
184  
185  
186  
187  
188  
189  
190  
191  
192  
193  
194  
195  
196  
197  
198  
199  
200  
201  
202  
203  
204  
205  
206  
207  
208  
209  
210  
211  
212  
213  
214  
215  
216  
217  
218  
219  
220  
221  
222  
223  
224  
225  
226  
227  
228  
229  
230  
231  
232  
233  
234  
235  
236  
237  
238  
239  
240  
241  
242  
243  
244  
245  
246  
247  
248  
249  
250  
251  
252  
253  
254  
255  
256  
257  
258  
259  
260  
261  
262  
263  
264  
265  
266  
267  
268  
269  
270  
271  
272  
273  
274  
275  
276  
277  
278  
279  
280  
281  
282  
283  
284  
285  
286  
287  
288  
289  
290  
291  
292  
293



				165					170					175			
Val	Val	Val	His	Ala	Cys	Arg	Asn	Leu	Ile	Ala	Phe	Ser	Glu	Asp	Gly		
			180					185					190				
Ser	Asp	Pro	Tyr	Val	Arg	Met	Tyr	Leu	Leu	Pro	Asp	Lys	Arg	Arg	Ser		
		195					200					205					
Gly	Arg	Arg	Lys	Thr	His	Val	Ser	Lys	Lys	Thr	Leu	Asn	Pro	Val	Phe		
	210					215					220						
Asp	Gln	Ser	Phe	Asp	Phe	Ser	Val	Ser	Leu	Pro	Glu	Val	Gln	Arg	Arg		
225					230					235					240		
Thr	Leu	Asp	Val	Ala	Val	Lys	Asn	Ser	Gly	Gly	Phe	Leu	Ser	Lys	Asp		
			245						250					255			
Lys	Gly	Leu	Leu	Gly	Lys	Val	Leu	Val	Ala	Leu	Ala	Ser	Glu	Glu	Leu		
		260					265						270				
Ala	Lys	Gly	Trp	Thr	Gln	Trp	Tyr	Asp	Leu	Thr	Glu	Asp	Gly	Thr	Arg		
		275					280					285					
Pro	Gln	Ala	Met	Thr													
	290																

## (2) INFORMATION FOR SEQ ID NO:23:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: None

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Met	Glu	Arg	Arg	His	Pro	Val	Cys	Ser	Gly	Thr	Cys	Gln	Pro	Thr	Gln		
1				5					10					15			
Phe	Arg	Cys	Ser	Asn	Gly	Cys	Cys	Ile	Asp	Ser	Phe	Leu	Glu	Cys	Asp		
		20						25				30					
Asp	Thr	Pro	Asn	Cys	Pro	Asp	Ala	Ser	Asp	Glu	Ala	Ala	Cys	Glu	Lys		
		35					40					45					
Tyr	Thr	Ser	Gly	Phe	Asp	Glu	Leu	Gln	Arg	Ile	His	Phe	Pro	Ser	Asp		
	50					55				60							
Lys	Gly	His	Cys	Val	Asp	Leu	Pro	Asp	Thr	Gly	Leu	Cys	Lys	Glu	Ser		
65				70						75				80			
Ile	Pro	Arg	Trp	Tyr	Tyr	Asn	Pro	Phe	Ser	Glu	His	Cys	Ala	Arg	Phe		
			85						90					95			
Thr	Tyr	Gly	Gly	Cys	Tyr	Gly	Asn	Lys	Asn	Asn	Phe	Glu	Glu	Glu	Gln		
		100					105						110				
Gln	Cys	Leu	Glu	Ser	Cys	Arg	Gly	Ile	Ser	Lys	Lys	Asp	Val	Phe	Gly		
	115						120					125					
Leu	Arg	Arg	Glu	Ile	Pro	Ile	Pro	Ser	Thr	Gly	Ser	Val	Glu	Met	Ala		
	130					135					140						
Val	Ala	Val	Phe	Leu	Val	Ile	Cys	Ile	Val	Val	Val	Val	Ala	Ile	Leu		
145					150					155					160		
Gly	Tyr	Cys	Phe	Phe	Lys	Asn	Gln	Arg	Lys	Asp	Phe	His	Gly	His	His		
			165						170					175			
His	His	Pro	Pro	Thr	Pro	Ala	Ser	Ser	Thr	Val	Ser	Thr	Thr	Glu			
		180					185					190					
Asp	Thr	Glu	His	Leu	Val	Tyr	Asn	His	Thr	Thr	Arg	Pro	Leu				
	195						200					205					

## (2) INFORMATION FOR SEQ ID NO:24:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 220 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: None

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Met Ala Gly Leu Ser Arg Gly Ser Ala Arg Ala Leu Leu Ala Ala Leu  
 1 5 10 15  
 Leu Ala Ser Thr Leu Leu Ala Leu Leu Val Ser Pro Ala Arg Gly Arg  
 20 25 30  
 Gly Gly Arg Asp His Gly Asp Trp Asp Glu Ala Ser Arg Leu Pro Pro  
 35 40 45  
 Leu Pro Pro Arg Glu Asp Ala Ala Arg Val Ala Arg Phe Val Thr His  
 50 55 60  
 Val Ser Asp Trp Gly Ala Leu Ala Thr Ile Ser Thr Leu Glu Ala Val  
 65 70 75 80  
 Arg Gly Arg Pro Phe Ala Asp Val Leu Ser Leu Ser Asp Gly Pro Pro  
 85 90 95  
 Gly Ala Gly Ser Gly Val Pro Tyr Phe Tyr Leu Ser Pro Leu Gln Leu  
 100 105 110  
 Ser Val Ser Asn Leu Gln Glu Asn Pro Tyr Ala Thr Leu Thr Met Thr  
 115 120 125  
 Leu Ala Gln Thr Asn Phe Cys Lys Lys His Gly Phe Asp Pro Gln Ser  
 130 135 140  
 Pro Leu Cys Val His Ile Met Leu Ser Gly Thr Val Thr Lys Val Asn  
 145 150 155 160  
 Glu Thr Glu Met Asp Ile Ala Lys His Ser Leu Phe Ile Arg His Pro  
 165 170 175  
 Glu Met Lys Thr Trp Pro Ser Ser His Asn Trp Phe Phe Ala Lys Leu  
 180 185 190  
 Asn Ile Thr Asn Ile Trp Val Leu Asp Tyr Phe Gly Gly Pro Lys Ile  
 195 200 205  
 Val Thr Pro Glu Glu Tyr Tyr Asn Val Thr Val Gln  
 210 215 220

## (2) INFORMATION FOR SEQ ID NO:25:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: None

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Met Asp His His Cys Pro Trp Leu Asn Asn Cys Val Gly His Tyr Asn  
 1 5 10 15  
 His Arg Tyr Phe Phe Ser Phe Cys Phe Phe Met Thr Leu Gly Cys Val  
 20 25 30

Tyr Cys Ser Tyr Gly Ser Trp Asp Leu Phe Arg Glu Ala Tyr Ala Ala  
 35 40 45  
 Ile Glu Lys Met Lys Gln Leu Asp Lys Asn Lys Leu Gln Ala Val Ala  
 50 55 60  
 Asn Gln Thr Tyr His Gln Thr Pro Pro Pro Thr Phe Ser Phe Arg Glu  
 65 70 75 80  
 Arg Met Thr His Lys Ser Leu Val Tyr Leu Trp Phe Leu Cys Ser Ser  
 85 90 95  
 Val Ala Leu Ala Leu Gly Ala Leu Thr Val Trp His Ala Val Leu Ile  
 100 105 110  
 Ser Arg Gly Glu Thr Ser Ile Glu Arg His Ile Asn Lys Lys Glu Arg  
 115 120 125  
 Arg Arg Leu Gln Ala Lys Gly Arg Val Phe Arg Asn Pro Tyr Asn Tyr  
 130 135 140  
 Gly Cys Leu Asp Asn Trp Lys Val Phe Leu Gly Val Asp Thr Gly Arg  
 145 150 155 160  
 His Trp Leu Thr Arg Val Leu Leu Pro Ser Thr His Leu Pro His Gly  
 165 170 175  
 Asn Gly Met Ser Trp Glu Pro Pro Pro Trp Val Thr Ala His Ser Ala  
 180 185 190  
 Ser Val Met Ala Val  
 195

## (2) INFORMATION FOR SEQ ID NO:26:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 451 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: None

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Met Ala Pro Leu Gly Met Leu Leu Gly Leu Leu Met Ala Ala Cys Phe  
 1 5 10 15  
 Thr Phe Cys Leu Ser His Gln Asn Leu Lys Glu Phe Ala Leu Thr Asn  
 20 25 30  
 Pro Glu Lys Ser Ser Thr Lys Glu Thr Glu Arg Lys Glu Thr Lys Ala  
 35 40 45  
 Glu Glu Glu Leu Asp Ala Glu Val Leu Glu Val Phe His Pro Thr His  
 50 55 60  
 Glu Trp Gln Ala Leu Gln Pro Gly Gln Ala Val Pro Ala Gly Ser His  
 65 70 75 80  
 Val Arg Leu Asn Leu Gln Thr Gly Glu Arg Glu Ala Lys Leu Gln Tyr  
 85 90 95  
 Glu Asp Lys Phe Arg Asn Asn Leu Lys Gly Lys Arg Leu Asp Ile Asn  
 100 105 110  
 Thr Asn Thr Tyr Thr Ser Gln Asp Leu Lys Ser Ala Leu Ala Lys Phe  
 115 120 125  
 Lys Glu Gly Ala Glu Met Glu Ser Ser Lys Glu Asp Lys Ala Arg Gln  
 130 135 140  
 Ala Glu Val Lys Arg Leu Phe Arg Pro Ile Glu Glu Leu Lys Lys Asp  
 145 150 155 160  
 Phe Asp Glu Leu Asn Val Val Ile Glu Thr Asp Met Gln Ile Met Val  
 165 170 175

1  
 2  
 3  
 4  
 5  
 6  
 7  
 8  
 9  
 10  
 11  
 12  
 13  
 14  
 15  
 16  
 17  
 18  
 19  
 20  
 21  
 22  
 23  
 24  
 25  
 26  
 27  
 28  
 29  
 30  
 31  
 32  
 33  
 34  
 35  
 36  
 37  
 38  
 39  
 40  
 41  
 42  
 43  
 44  
 45  
 46  
 47  
 48  
 49  
 50  
 51  
 52  
 53  
 54  
 55  
 56  
 57  
 58  
 59  
 60  
 61  
 62  
 63  
 64  
 65  
 66  
 67  
 68  
 69  
 70  
 71  
 72  
 73  
 74  
 75  
 76  
 77  
 78  
 79  
 80  
 81  
 82  
 83  
 84  
 85  
 86  
 87  
 88  
 89  
 90  
 91  
 92  
 93  
 94  
 95  
 96  
 97  
 98  
 99  
 100  
 101  
 102  
 103  
 104  
 105  
 106  
 107  
 108  
 109  
 110  
 111  
 112  
 113  
 114  
 115  
 116  
 117  
 118  
 119  
 120  
 121  
 122  
 123  
 124  
 125  
 126  
 127  
 128  
 129  
 130  
 131  
 132  
 133  
 134  
 135  
 136  
 137  
 138  
 139  
 140  
 141  
 142  
 143  
 144  
 145  
 146  
 147  
 148  
 149  
 150  
 151  
 152  
 153  
 154  
 155  
 156  
 157  
 158  
 159  
 160  
 161  
 162  
 163  
 164  
 165  
 166  
 167  
 168  
 169  
 170  
 171  
 172  
 173  
 174  
 175  
 176  
 177  
 178  
 179  
 180  
 181  
 182  
 183  
 184  
 185  
 186  
 187  
 188  
 189  
 190  
 191  
 192  
 193  
 194  
 195  
 196  
 197  
 198  
 199  
 200  
 201  
 202  
 203  
 204  
 205  
 206  
 207  
 208  
 209  
 210  
 211  
 212  
 213  
 214  
 215  
 216  
 217  
 218  
 219  
 220  
 221  
 222  
 223  
 224  
 225  
 226  
 227  
 228  
 229  
 230  
 231  
 232  
 233  
 234  
 235  
 236  
 237  
 238  
 239  
 240  
 241  
 242  
 243  
 244  
 245  
 246  
 247  
 248  
 249  
 250  
 251  
 252  
 253  
 254  
 255  
 256  
 257  
 258  
 259  
 260  
 261  
 262  
 263  
 264  
 265  
 266  
 267  
 268  
 269  
 270  
 271  
 272  
 273  
 274  
 275  
 276  
 277  
 278  
 279  
 280  
 281  
 282  
 283  
 284  
 285  
 286  
 287  
 288  
 289  
 290  
 291  
 292  
 293  
 294  
 295  
 296  
 297  
 298  
 299  
 300  
 301  
 302  
 303  
 304  
 305  
 306  
 307  
 308  
 309  
 310  
 311  
 312  
 313  
 314  
 315  
 316  
 317  
 318  
 319  
 320  
 321  
 322  
 323  
 324  
 325  
 326  
 327  
 328  
 329  
 330  
 331  
 332  
 333  
 334  
 335  
 336  
 337  
 338  
 339  
 340  
 341  
 342  
 343  
 344  
 345  
 346  
 347  
 348  
 349  
 350  
 351  
 352  
 353  
 354  
 355  
 356  
 357  
 358  
 359  
 360  
 361  
 362  
 363  
 364  
 365  
 366  
 367  
 368  
 369  
 370  
 371  
 372  
 373  
 374  
 375  
 376  
 377  
 378  
 379  
 380  
 381  
 382  
 383  
 384  
 385  
 386  
 387  
 388  
 389  
 390  
 391  
 392  
 393  
 394  
 395  
 396  
 397  
 398  
 399  
 400  
 401  
 402  
 403  
 404  
 405  
 406  
 407  
 408  
 409  
 410  
 411  
 412  
 413  
 414  
 415  
 416  
 417  
 418  
 419  
 420  
 421  
 422  
 423  
 424  
 425  
 426  
 427  
 428  
 429  
 430  
 431  
 432  
 433  
 434  
 435  
 436  
 437  
 438  
 439  
 440  
 441  
 442  
 443  
 444  
 445  
 446  
 447  
 448  
 449  
 450  
 451  
 452  
 453  
 454  
 455  
 456  
 457  
 458  
 459  
 460  
 461  
 462  
 463  
 464  
 465  
 466  
 467  
 468  
 469  
 470  
 471  
 472  
 473  
 474  
 475  
 476  
 477  
 478  
 479  
 480  
 481  
 482  
 483  
 484  
 485  
 486  
 487  
 488  
 489  
 490  
 491  
 492  
 493  
 494  
 495  
 496  
 497  
 498  
 499  
 500  
 501  
 502  
 503  
 504  
 505  
 506  
 507  
 508  
 509  
 510  
 511  
 512  
 513  
 514  
 515  
 516  
 517  
 518  
 519  
 520  
 521  
 522  
 523  
 524  
 525  
 526  
 527  
 528  
 529  
 530  
 531  
 532  
 533  
 534  
 535  
 536  
 537  
 538  
 539  
 540  
 541  
 542  
 543  
 544  
 545  
 546  
 547  
 548  
 549  
 550  
 551  
 552  
 553  
 554  
 555  
 556  
 557  
 558  
 559  
 560  
 561  
 562  
 563  
 564  
 565  
 566  
 567  
 568  
 569  
 570  
 571  
 572  
 573  
 574  
 575  
 576  
 577  
 578  
 579  
 580  
 581  
 582  
 583  
 584  
 585  
 586  
 587  
 588  
 589  
 590  
 591  
 592  
 593  
 594  
 595  
 596  
 597  
 598  
 599  
 600  
 601  
 602  
 603  
 604  
 605  
 606  
 607  
 608  
 609  
 610  
 611  
 612  
 613  
 614  
 615  
 616  
 617  
 618  
 619  
 620  
 621  
 622  
 623  
 624  
 625  
 626  
 627  
 628  
 629  
 630  
 631  
 632  
 633  
 634  
 635  
 636  
 637  
 638  
 639  
 640  
 641  
 642  
 643  
 644  
 645  
 646  
 647  
 648  
 649  
 650  
 651  
 652  
 653  
 654  
 655  
 656  
 657  
 658  
 659  
 660  
 661  
 662  
 663  
 664  
 665  
 666  
 667  
 668  
 669  
 670  
 671  
 672  
 673  
 674  
 675  
 676  
 677  
 678  
 679  
 680  
 681  
 682  
 683  
 684  
 685  
 686  
 687  
 688  
 689  
 690  
 691  
 692  
 693  
 694  
 695  
 696  
 697  
 698  
 699  
 700  
 701  
 702  
 703  
 704  
 705  
 706  
 707  
 708  
 709  
 710  
 711  
 712  
 713  
 714  
 715  
 716  
 717  
 718  
 719  
 720  
 721  
 722  
 723  
 724  
 725  
 726  
 727  
 728  
 729  
 730  
 731  
 732  
 733  
 734  
 735  
 736  
 737  
 738  
 739  
 740  
 741  
 742  
 743  
 744  
 745  
 746  
 747  
 748  
 749  
 750  
 751  
 752  
 753  
 754  
 755  
 756  
 757  
 758  
 759  
 760  
 761  
 762  
 763  
 764  
 765  
 766  
 767  
 768  
 769  
 770  
 771  
 772  
 773  
 774  
 775  
 776  
 777  
 778  
 779  
 780  
 781  
 782  
 783  
 784  
 785  
 786  
 787  
 788  
 789  
 790  
 791  
 792  
 793  
 794  
 795  
 796  
 797  
 798  
 799  
 800  
 801  
 802  
 803  
 804  
 805  
 806  
 807  
 808  
 809  
 810  
 811  
 812  
 813  
 814  
 815  
 816  
 817  
 818  
 819  
 820  
 821  
 822  
 823  
 824  
 825  
 826  
 827  
 828  
 829  
 830  
 831  
 832  
 833  
 834  
 835  
 836  
 837  
 838  
 839  
 840  
 841  
 842  
 843  
 844  
 845  
 846  
 847  
 848  
 849  
 850  
 851  
 852  
 853  
 854  
 855  
 856  
 857  
 858  
 859  
 860  
 861  
 862  
 863  
 864  
 865  
 866  
 867  
 868  
 869  
 870  
 871  
 872  
 873  
 874  
 875  
 876  
 877  
 878  
 879  
 880  
 881  
 882  
 883  
 884  
 885  
 886  
 887  
 888  
 889  
 890  
 891  
 892  
 893  
 894  
 895  
 896  
 897  
 898  
 899  
 900  
 901  
 902  
 903  
 904  
 905  
 906  
 907  
 908  
 909  
 910  
 911  
 912  
 913  
 914  
 915  
 916  
 917  
 918  
 919  
 920  
 921  
 922  
 923  
 924  
 925  
 926  
 927  
 928  
 929  
 930  
 931  
 932  
 933  
 934  
 935  
 936  
 937  
 938  
 939  
 940  
 941  
 942  
 943  
 944  
 945  
 946  
 947  
 948  
 949  
 950  
 951  
 952  
 953  
 954  
 955  
 956  
 957  
 958  
 959  
 960  
 961  
 962  
 963  
 964  
 965  
 966  
 967  
 968  
 969  
 970  
 971  
 972  
 973  
 974  
 975  
 976  
 977  
 978  
 979  
 980  
 981  
 982  
 983  
 984  
 985  
 986  
 987  
 988  
 989  
 990  
 991  
 992  
 993  
 994  
 995  
 996  
 997  
 998  
 999  
 1000  
 1001  
 1002  
 1003  
 1004  
 1005  
 1006  
 1007  
 1008  
 1009  
 1010  
 1011  
 1012  
 1013  
 1014  
 1015  
 1016  
 1017  
 1018  
 1019  
 1020  
 1021  
 1022  
 1023  
 1024  
 1025  
 1026  
 1027  
 1028  
 1029  
 1030  
 1031  
 1032  
 1033  
 1034  
 1035  
 1036  
 1037  
 1038  
 1039  
 1040  
 1041  
 1042  
 1043  
 1044  
 1045  
 1046  
 1047  
 1048  
 1049  
 1050  
 1051  
 1052  
 1053  
 1054  
 1055  
 1056  
 1057  
 1058  
 1059  
 1060  
 1061  
 1062  
 1063  
 1064  
 1065  
 1066  
 1067  
 1068  
 1069  
 1070  
 1071  
 1072  
 1073  
 1074  
 1075  
 1076  
 1077  
 1078  
 1079  
 1080  
 1081  
 1082  
 1083  
 1084  
 1085  
 1086  
 1087  
 1088  
 1089  
 1090  
 1091  
 1092  
 1093  
 1094  
 1095  
 1096  
 1097  
 1098  
 1099  
 1100  
 1101  
 1102  
 1103  
 1104  
 1105  
 1106  
 1107  
 1108  
 1109  
 1110  
 1111  
 1112  
 1113  
 1114  
 1115  
 1116  
 1117  
 1118  
 1119  
 1120  
 1121  
 1122  
 1123  
 1124  
 1125  
 1126  
 1127  
 1128  
 1129  
 1130  
 1131  
 1132  
 1133  
 1134  
 1135  
 1136  
 1137  
 1138  
 1139  
 1140  
 1141  
 1142  
 1143  
 1144  
 1145  
 1146  
 1147  
 1148  
 1149  
 1150  
 1151  
 1152  
 1153  
 1154  
 1155  
 1156  
 1157  
 1158  
 1159  
 1160  
 1161  
 1162  
 1163  
 1164  
 1165  
 1166  
 1167  
 1168  
 1169  
 1170  
 1171  
 1172  
 1173  
 1174  
 1175  
 1176  
 1177  
 1178  
 1179  
 1180  
 1181  
 1182  
 1183  
 1184  
 1185  
 1186  
 1187  
 1188  
 1189  
 1190  
 1191  
 1192  
 1193  
 1194  
 1195  
 1196  
 1197  
 1198  
 1199  
 1200  
 1201  
 1202  
 1203  
 1204  
 1205  
 1206  
 1207  
 1208  
 1209  
 1210  
 1211  
 1212  
 1213  
 1214  
 1215  
 1216  
 1217  
 1218  
 1219  
 1220  
 1221  
 1222  
 1223  
 1224  
 1225  
 1226  
 1227  
 1228  
 1229  
 1230  
 1231  
 1232  
 1233  
 1234  
 1235  
 1236  
 1237  
 1238  
 1239  
 1240  
 1241  
 1242  
 1243  
 1244  
 1245  
 1246  
 1247  
 1248  
 1249  
 1250  
 1251  
 1252  
 1253  
 1254  
 1255  
 1256  
 1257  
 1258  
 1259  
 1260  
 1261  
 1262  
 1263  
 1264  
 1265  
 1266  
 1267  
 1268  
 1269  
 1270  
 1271  
 1272  
 1273  
 1274  
 1275  
 1276  
 1277  
 1278  
 1279  
 1280  
 1281  
 1282  
 1283  
 1284  
 1285  
 1286  
 1287  
 1288  
 1289  
 1290  
 1291  
 1292  
 1293  
 1294  
 1295  
 1296  
 1297  
 1298  
 1299  
 1300  
 1301  
 1302  
 1303  
 1304  
 1305  
 1306  
 1307  
 1308  
 1309  
 1310  
 1311  
 1312  
 1313  
 1314  
 1315  
 1316  
 1317  
 1318  
 1319  
 1320  
 1321  
 1322  
 1323  
 1324  
 1325  
 1326  
 1327  
 1328  
 1329  
 1330  
 1331  
 1332  
 1333  
 1334  
 1335  
 1336  
 1337  
 1338  
 1339  
 1340  
 1341  
 1342  
 1343  
 1344  
 1345  
 1346  
 1347  
 1348  
 1349  
 1350  
 1351  
 1352  
 1353  
 1354

Arg Leu Ile Asn Lys Phe Asn Ser Ser Ser Ser Ser Leu Glu Glu Lys  
 180 185 190  
 Ile Ala Ala Leu Phe Asp Leu Glu Tyr Tyr Val His Gln Met Asp Asn  
 195 200 205  
 Ala Gln Asp Leu Leu Ser Phe Gly Gly Leu Gln Val Val Ile Asn Gly  
 210 215 220  
 Leu Asn Ser Thr Glu Pro Leu Val Lys Glu Tyr Ala Ala Phe Val Leu  
 225 230 235 240  
 Gly Ala Ala Phe Ser Ser Asn Pro Lys Val Gln Val Glu Ala Ile Glu  
 245 250 255  
 Gly Gly Ala Leu Gln Lys Leu Leu Val Ile Leu Ala Thr Glu Gln Pro  
 260 265 270  
 Leu Thr Ala Lys Lys Lys Val Leu Phe Ala Leu Cys Ser Leu Leu Arg  
 275 280 285  
 His Phe Pro Tyr Ala Gln Arg Gln Phe Leu Lys Leu Gly Gly Leu Gln  
 290 295 300  
 Val Leu Arg Thr Leu Val Gln Glu Lys Gly Thr Glu Val Leu Ala Val  
 305 310 315 320  
 Arg Val Val Thr Leu Leu Tyr Asp Leu Val Thr Glu Lys Met Phe Ala  
 325 330 335  
 Glu Glu Glu Ala Glu Leu Thr Gln Glu Met Ser Pro Glu Lys Leu Gln  
 340 345 350  
 Gln Tyr Arg Gln Val His Leu Leu Pro Gly Leu Trp Glu Gln Gly Trp  
 355 360 365  
 Cys Glu Ile Thr Ala His Leu Leu Ala Leu Pro Glu His Asp Ala Arg  
 370 375 380  
 Glu Lys Val Leu Gln Thr Leu Gly Val Leu Leu Thr Thr Cys Arg Asp  
 385 390 395 400  
 Arg Tyr Arg Gln Asp Pro Gln Leu Gly Arg Thr Leu Ala Ser Leu Gln  
 405 410 415  
 Ala Glu Tyr Gln Val Leu Ala Ser Leu Glu Leu Gln Asp Gly Glu Asp  
 420 425 430  
 Glu Gly Tyr Phe Gln Glu Leu Leu Gly Ser Val Asn Ser Leu Leu Lys  
 435 440 445  
 Glu Leu Arg  
 450

## (2) INFORMATION FOR SEQ ID NO:27:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: None

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Met Trp Gln Ala Gly Lys Arg Gln Ala Ser Arg Ala Phe Ser Leu Tyr  
 1 5 10 15  
 Ala Asn Ile Asp Ile Leu Arg Pro Tyr Phe Asp Val Glu Pro Ala Gln  
 20 25 30  
 Val Arg Ser Arg Leu Leu Glu Ser Met Ile Pro Ile Lys Met Val Asn  
 35 40 45  
 Phe Pro Gln Lys Ile Ala Gly Glu Leu Tyr Gly Pro Leu Met Leu Val  
 50 55 60

Phe Thr Leu Val Ala Ile Leu Leu His Gly Met Lys Thr Ser Asp Thr  
 65 70 75 80  
 Ile Ile Arg Glu Gly Thr Leu Met Gly Thr Ala Ile Gly Thr Cys Phe  
 85 90 95  
 Gly Tyr Trp Leu Gly Val Ser Ser Phe Ile Tyr Phe Leu Ala Tyr Leu  
 100 105 110  
 Cys Asn Ala Gln Ile Thr Met Leu Gln Met Leu Ala Leu Leu Gly Tyr  
 115 120 125  
 Gly Leu Phe Gly His Cys Ile Val Leu Phe Ile Thr Tyr Asn Ile His  
 130 135 140  
 Leu His Ala Leu Phe Tyr Leu Phe Trp Leu Leu Val Gly Gly Leu Ser  
 145 150 155 160  
 Thr Leu Arg Met Val Ala Val Leu Val Ser Arg Thr Val Gly Pro Thr  
 165 170 175  
 Gln Arg Leu Leu Leu Cys Gly Thr Leu Ala Ala Leu His Met Leu Phe  
 180 185 190  
 Leu Leu Tyr Leu His Phe Ala Tyr His Lys Val Val Glu Gly Ile Leu  
 195 200 205  
 Asp Thr Leu Glu Gly Pro Asn Ile Pro Pro Ile Gln Arg Val Pro Arg  
 210 215 220  
 Asp Ile Pro Ala Met Leu Pro Ala Ala Arg Leu Pro Thr Thr Val Leu  
 225 230 235 240  
 Asn Ala Thr Ala Lys Ala Val Ala Val Thr Leu Gln Ser His  
 245 250

## (2) INFORMATION FOR SEQ ID NO:28:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 221 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: None

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Met Gly Ser Glu Asn Glu Ala Leu Asp Leu Ser Met Lys Ser Val Pro  
 1 5 10 15  
 Trp Leu Lys Ala Gly Glu Val Ser Pro Pro Ile Phe Gln Glu Asp Ala  
 20 25 30  
 Ala Leu Asp Leu Ser Val Ala Ala His Arg Lys Ser Glu Pro Pro Pro  
 35 40 45  
 Glu Thr Leu Tyr Asp Ser Gly Ala Ser Val Asp Ser Ser Gly His Thr  
 50 55 60  
 Val Met Glu Lys Leu Pro Ser Gly Met Glu Ile Ser Phe Ala Pro Ala  
 65 70 75 80  
 Thr Ser His Glu Ala Pro Ala Met Met Asp Ser His Ile Ser Ser Ser  
 85 90 95  
 Asp Ala Ala Thr Glu Met Leu Ser Gln Pro Asn His Pro Ser Gly Glu  
 100 105 110  
 Val Lys Ala Glu Asn Asn Ile Glu Met Val Gly Glu Ser Gln Ala Ala  
 115 120 125  
 Lys Val Ile Val Ser Val Glu Asp Ala Val Pro Thr Ile Phe Cys Gly  
 130 135 140  
 Lys Ile Lys Gly Leu Ser Gly Val Ser Thr Lys Asn Phe Ser Phe Lys  
 145 150 155 160

PHE THR LEU VAL ALA ILE LEU LEU HIS GLY MET LYS THR SER ASP THR  
 65 70 75 80  
 ILE ILE ARG GLU GLY THR LEU MET GLY THR ALA ILE GLY THR CYS PHE  
 85 90 95  
 GLY TYR TRP LEU GLY VAL SER SER PHE ILE TYR PHE LEU ALA TYR LEU  
 100 105 110  
 CYS ASN ALA GLN ILE THR MET LEU GLN MET LEU ALA LEU LEU GLY TYR  
 115 120 125  
 GLY LEU PHE GLY HIS CYS ILE VAL LEU PHE ILE THR TYR ASN ILE HIS  
 130 135 140  
 LEU HIS ALA LEU PHE TYR LEU PHE TRP LEU LEU VAL GLY GLY LEU SER  
 145 150 155 160  
 THR LEU ARG MET VAL ALA VAL LEU VAL SER ARG THR VAL GLY PRO THR  
 165 170 175  
 GLN ARG LEU LEU LEU CYS GLY THR LEU ALA ALA LEU HIS MET LEU PHE  
 180 185 190  
 LEU LEU TYR LEU HIS PHE ALA TYR HIS LYS VAL VAL GLU GLY ILE LEU  
 195 200 205  
 ASP THR LEU GLU GLY PRO ASN ILE PRO PRO ILE GLN ARG VAL PRO ARG  
 210 215 220  
 ASP ILE PRO ALA MET LEU PRO ALA ALA ARG LEU PRO THR THR VAL LEU  
 225 230 235 240  
 ASN ALA THR ALA LYS ALA VAL ALA VAL THR LEU GLN SER HIS  
 245 250

Arg	Glu	Asp	Ser	Val	Leu	Gln	Gly	Tyr	Asp	Ile	Asn	Ser	Gln	Gly	Glu
				165					170					175	
Glu	Ser	Met	Gly	Asn	Ala	Glu	Pro	Leu	Arg	Lys	Pro	Ile	Lys	Asn	Arg
			180					185					190		
Ser	Ile	Lys	Leu	Lys	Lys	Val	Asn	Ser	Gln	Glu	Val	His	Met	Leu	Pro
		195					200					205			
Ile	Lys	Lys	Gln	Arg	Leu	Ala	Thr	Phe	Phe	Pro	Arg	Lys			
	210					215					220				

## (2) INFORMATION FOR SEQ ID NO:29:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: None

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Met	Val	Lys	Val	Thr	Phe	Asn	Ser	Ala	Leu	Ala	Gln	Lys	Glu	Ala	Lys
1				5					10					15	
Lys	Asp	Glu	Pro	Lys	Ser	Gly	Glu	Glu	Ala	Leu	Ile	Ile	Pro	Pro	Asp
			20					25					30		
Ala	Val	Ala	Val	Asp	Cys	Lys	Asp	Pro	Asp	Asp	Val	Val	Pro	Val	Gly
		35					40					45			
Gln	Arg	Arg	Ala	Trp	Cys	Trp	Cys	Met	Cys	Phe	Gly	Leu	Ala	Phe	Met
	50					55					60				
Leu	Ala	Gly	Val	Ile	Leu	Gly	Gly	Ala	Tyr	Leu	Tyr	Lys	Tyr	Phe	Ala
	65				70				75						80
Leu	Gln	Pro	Asp	Asp	Val	Tyr	Tyr	Cys	Gly	Ile	Lys	Tyr	Ile	Lys	Asp
			85						90					95	
Asp	Val	Ile	Leu	Asn	Glu	Pro	Ser	Ala	Asp	Ala	Pro	Ala	Ala	Leu	Tyr
			100					105					110		
Gln	Thr	Ile	Glu	Glu	Asn	Ile	Lys	Ile	Phe	Glu	Glu	Glu	Glu	Val	Glu
		115					120					125			
Phe	Ile	Ser	Val	Pro	Val	Pro	Glu	Phe	Ala	Asp	Ser	Asp	Pro	Ala	Asn
	130					135					140				
Ile	Val	His	Asp	Phe	Asn	Lys	Lys	Leu	Thr	Ala	Tyr	Leu	Asp	Leu	Asn
	145				150					155					160
Leu	Asp	Lys	Cys	Tyr	Val	Ile	Pro	Leu	Asn	Thr	Ser	Ile	Val	Met	Pro
			165						170					175	
Pro	Arg	Asn	Leu	Leu	Glu	Leu	Leu	Ile	Asn	Ile	Lys	Ala	Gly	Thr	Tyr
			180					185					190		
Leu	Pro	Gln	Ser	Tyr	Leu	Ile	His	Glu	His	Met	Val	Ile	Thr	Asp	Arg
		195					200					205			
Ile	Glu	Asn	Ile	Asp	His	Leu	Gly	Phe	Phe	Ile	Tyr	Arg	Leu	Cys	His
	210					215					220				
Asp	Lys	Glu	Thr	Tyr	Lys	Leu	Gln	Arg	Arg	Glu	Thr	Ile	Lys	Gly	Ile
	225				230					235					240
Gln	Lys	Arg	Glu	Ala	Ser	Asn	Cys	Phe	Ala	Ile	Arg	His	Phe	Glu	Asn
				245					250					255	
Lys	Phe	Ala	Val	Glu	Thr	Leu	Ile	Cys	Ser						
			260					265							

## (2) INFORMATION FOR SEQ ID NO:30:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: None

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

```

Met Pro Thr Gly Asp Phe Asp Ser Lys Pro Ser Trp Ala Asp Gln Val
 1          5          10          15
Glu Glu Glu Gly Glu Asp Asp Lys Cys Val Thr Ser Glu Leu Leu Lys
 20          25          30
Gly Ile Pro Leu Ala Thr Gly Asp Thr Ser Pro Glu Pro Glu Leu Leu
 35          40          45
Pro Gly Ala Pro Leu Pro Pro Lys Glu Val Ile Asn Gly Asn Ile
 50          55          60
Lys Thr Val Thr Glu Tyr Lys Ile Asp Glu Asp Gly Lys Lys Phe Lys
 65          70          75          80
Ile Val Arg Thr Phe Arg Ile Glu Thr Arg Lys Ala Ser Lys Ala Val
 85          90          95
Ala Arg Arg Lys Asn Trp Lys Lys Phe Gly Asn Ser Glu Phe Asp Pro
 100          105          110
Pro Gly Pro Asn Val Ala Thr Thr Thr Val Ser Asp Asp Val Ser Met
 115          120          125
Thr Phe Ile Thr Ser Lys Glu Asp Leu Asn Cys Gln Glu Glu Glu Asp
 130          135          140
Pro Met Asn Lys Phe Lys Gly Gln Lys Ile Val Ser Cys Arg Ile Cys
 145          150          155          160
Lys Gly Asp His Trp Thr Thr Arg Cys Pro Tyr Lys Asp Thr Leu Gly
 165          170          175
Pro Met Gln Lys Glu Leu Ala Glu Gln Leu Gly Leu Ser Thr Gly Glu
 180          185          190
Lys Glu Lys Leu Pro Gly Glu Leu Glu Pro Val Gln Ala Thr Gln Asn
 195          200          205
Lys Thr Gly Lys Tyr Val Pro Pro Ser Leu Arg Asp Gly Ala Ser Arg
 210          215          220
Arg Gly Glu Ser Met Gln Pro Asn Arg Arg Ala Asp Asp Asn Ala Thr
 225          230          235          240
Ile Arg Val Thr Asn Leu Arg Arg Gly His Ala
 245          250

```

## (2) INFORMATION FOR SEQ ID NO:31:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: None

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Met Arg Arg Leu Asn Arg Lys Lys Thr Leu Ser Leu Val Lys Glu Leu

1	5	10	15
Asp Ala Phe	Pro Lys Val	Pro Glu Ser Tyr	Val Glu Thr Ser Ala Ser
	20	25	30
Gly Gly Thr	Val Ser Leu Ile	Ala Phe Thr Thr	Met Ala Leu Leu Thr
	35	40	45
Ile Met Glu	Phe Ser Val Tyr	Gln Asp Thr Trp	Met Lys Tyr Glu Tyr
	50	55	60
Glu Val Asp	Lys Asp Phe Ser	Ser Lys Leu Arg	Ile Asn Ile Asp Ile
	65	70	75
Thr Val Ala	Met Lys Cys Gln	Tyr Val Gly Ala	Asp Val Leu Asp Leu
	85	90	95
Ala Glu Thr	Met Val Ala Ser	Ala Asp Gly Leu	Val Tyr Glu Pro Thr
	100	105	110
Val Phe Asp	Leu Ser Pro Gln	Gln Lys Glu Trp	Gln Arg Met Leu Gln
	115	120	125
Leu Ile Gln	Ser Arg Leu Gln	Glu Glu His Ser	Leu Gln Asp Val Ile
	130	135	140
Phe Lys Ser	Ala Phe Lys Ser	Thr Ser Thr Ala	Leu Pro Pro Arg Glu
	145	150	155
Asp Asp Ser	Ser Gln Ser Pro	Asn Ala Cys Arg	Ile His Gly His Leu
	165	170	175
Tyr Val Asn	Lys Val Ala Gly	Asn Phe His Ile	Thr Val Gly Lys Ala
	180	185	190
Ile Pro His	Pro Arg Gly His	Ala His Leu Ala	Ala Leu Val Asn His
	195	200	205
Glu Ser Tyr	Asn Phe Ser His	Arg Ile Asp His	Leu Ser Phe Gly Glu
	210	215	220
Leu Val Pro	Ala Ile Ile Asn	Pro Leu Asp Gly	Thr Glu Lys Ile Ala
	225	230	235
Ile Asp His	Asn Gln Met Phe	Gln Tyr Phe Ile	Thr Val Val Pro Thr
	245	250	255
Lys Leu His	Thr Tyr Lys Ile	Ser Ala Asp Thr	His Gln Phe Ser Val
	260	265	270
Thr Glu Arg	Glu Arg Ile Ile	Asn His Ala Ala	Gly Ser His Gly Val
	275	280	285
Ser Gly Ile	Phe Met Lys Tyr	Asp Leu Ser Ser	Leu Met Val Thr Val
	290	295	300
Thr Glu Glu	His Met Pro Phe	Trp Gln Phe Phe	Val Arg Leu Cys Gly
	305	310	315
Ile Val Gly	Gly Ile Phe Ser	Thr Thr Gly Met	Leu His Gly Ile Gly
	325	330	335
Lys Phe Ile	Val Glu Ile Ile	Cys Cys Arg Phe	Arg Leu Gly Ser Tyr
	340	345	350
Lys Pro Val	Asn Ser Val Pro	Phe Glu Asp Gly	His Thr Asp Asn His
	355	360	365
Leu Pro Leu	Leu Glu Asn Asn	Thr His	
	370	375	

## (2) INFORMATION FOR SEQ ID NO:32:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: None



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Met Gly Ser Gln His Ser Ala Ala Ala Arg Pro Ser Ser Cys Arg Arg  
 1 5 10 15  
 Lys Gln Glu Asp Asp Arg Asp Gly Leu Leu Ala Glu Arg Glu Gln Glu  
 20 25 30  
 Glu Ala Ile Ala Gln Phe Pro Tyr Val Glu Phe Thr Gly Arg Asp Ser  
 35 40 45  
 Ile Thr Cys Leu Thr Cys Gln Gly Thr Gly Tyr Ile Pro Thr Glu Gln  
 50 55 60  
 Val Asn Glu Leu Val Ala Leu Ile Pro His Ser Asp Gln Arg Leu Arg  
 65 70 75 80  
 Pro Gln Arg Thr Lys Gln Tyr Val Leu Leu Ser Ile Leu Leu Cys Leu  
 85 90 95  
 Leu Ala Ser Gly Leu Val Val Phe Phe Leu Phe Pro His Ser Val Leu  
 100 105 110  
 Val Asp Asp Asp Gly Ile Lys Val Val Lys Val Thr Phe Asn Lys Gln  
 115 120 125  
 Asp Ser Leu Val Ile Leu Thr Ile Met Ala Thr Leu Lys Ile Arg Asn  
 130 135 140  
 Ser Asn Phe Tyr Thr Val Ala Val Thr Ser Leu Ser Ser Gln Ile Gln  
 145 150 155 160  
 Tyr Met Asn Thr Val Val Ser Thr Tyr Val Thr Thr Asn Val Ser Leu  
 165 170 175  
 Ile Pro Pro Arg Ser Glu Gln Leu Val Asn Phe Thr Gly Lys Ala Glu  
 180 185 190  
 Met Gly Gly Pro Phe Ser Tyr Val Tyr Phe Phe Cys Thr Val Pro Glu  
 195 200 205  
 Ile Leu Val His Asn Ile Val Ile Phe Met Arg Thr Ser Val Lys Ile  
 210 215 220  
 Ser Tyr Ile Gly Leu Met Thr Gln Ser Ser Leu Glu Thr His His Tyr  
 225 230 235 240  
 Val Asp Cys Gly Gly Asn Ser Thr Ala Ile  
 245 250

## (2) INFORMATION FOR SEQ ID NO:33:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: None

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Met Val Thr Cys Phe His Val Pro Tyr Ser Ala Leu Thr Met Phe Ile  
 1 5 10 15  
 Ser Thr Glu Gln Thr Glu Arg Asp Ser Ala Thr Ala Tyr Arg Met Thr  
 20 25 30  
 Val Glu Val Leu Gly Thr Val Leu Gly Thr Ala Ile Gln Gly Gln Ile  
 35 40 45  
 Val Gly Gln Ala Asp Thr Pro Cys Phe Gln Asp Leu Asn Ser Ser Thr  
 50 55 60  
 Val Ala Ser Gln Ser Ala Asn His Thr His Gly Thr Thr Ser His Arg

65 70 75 80  
 Glu Thr Gln Lys Ala Tyr Leu Leu Ala Ala Gly Val Ile Val Cys Ile  
 85 90 95  
 Tyr Ile Ile Cys Ala Val Ile Leu Ile Leu Gly Val Arg Glu Gln Arg  
 100 105 110  
 Glu Pro Tyr Glu Ala Gln Gln Ser Glu Pro Ile Ala Tyr Phe Arg Gly  
 115 120 125  
 Leu Arg Leu Val Met Ser His Gly Pro Tyr Ile Lys Leu Ile Thr Gly  
 130 135 140  
 Phe Leu Phe Thr Ser Leu Ala Phe Met Leu Val Glu Gly Asn Phe Val  
 145 150 155 160  
 Leu Phe Cys Thr Tyr Thr Leu Gly Phe Arg Asn Glu Phe Gln Asn Leu  
 165 170 175  
 Leu Leu Ala Ile Met Leu Ser Ala Thr Leu Thr Ile Pro Ile Trp Gln  
 180 185 190  
 Trp Phe Leu Thr Arg Phe Gly Lys Lys Thr Ala Val Tyr Val Gly Ile  
 195 200 205  
 Ser Ser Ala Val Pro Phe Leu Ile Leu Val Ala Leu Met Glu Ser Asn  
 210 215 220  
 Leu Ile Ile Thr Tyr Ala Val Ala Val Ala Ala Gly Ile Ser Val Ala  
 225 230 235 240  
 Ala Ala Phe Leu Leu Pro Trp Ser Met Leu Pro Asp Val Ile Asp Asp  
 245 250 255  
 Phe His Leu Lys Gln Pro His Phe His Gly Thr Glu Pro Ile Phe Phe  
 260 265 270  
 Ser Phe Tyr Val Phe Phe Thr Lys Phe Ala Ser Gly Val Ser Leu Gly  
 275 280 285  
 Ile Ser Thr Leu Ser Leu Asp Phe Ala Gly Tyr Gln Thr Arg Gly Cys  
 290 295 300  
 Ser Gln Pro Glu Arg Val Lys Phe Thr Leu Asn Met Leu Val Thr Met  
 305 310 315 320  
 Ala Pro Ile Val Leu Ile Leu Leu Gly Leu Leu Leu Phe Lys Met Tyr  
 325 330 335  
 Pro Ile Asp Glu Glu Arg Arg Arg Gln Asn Lys Lys Ala Leu Gln Ala  
 340 345 350  
 Leu Arg Asp Glu Ala Ser Ser Ser Gly Cys Ser Glu Thr Asp Ser Thr  
 355 360 365  
 Glu Leu Ala Ser Ile Leu  
 370

## (2) INFORMATION FOR SEQ ID NO:34:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: None

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Met Val Asn Asp Pro Pro Val Pro Ala Leu Leu Trp Ala Gln Glu Val  
 1 5 10 15  
 Gly Gln Val Leu Ala Gly Arg Ala Arg Arg Leu Leu Leu Gln Phe Gly  
 20 25 30  
 Val Leu Phe Cys Thr Ile Leu Leu Leu Leu Trp Val Ser Val Phe Leu

```

      35              40              45
Tyr Gly Ser Phe Tyr Tyr Ser Tyr Met Pro Thr Val Ser His Leu Ser
  50              55              60
Pro Val His Phe Tyr Tyr Arg Thr Asp Cys Asp Ser Ser Thr Thr Ser
  65              70              75              80
Leu Cys Ser Phe Pro Val Ala Asn Val Ser Leu Thr Lys Gly Gly Arg
      85              90              95
Asp Arg Val Leu Met Tyr Gly Gln Pro Tyr Arg Val Thr Leu Glu Leu
      100              105              110
Glu Leu Pro Glu Ser Pro Val Asn Gln Asp Leu Gly Met Phe Leu Val
      115              120              125
Thr Ile Ser Cys Tyr Thr Arg Gly Gly Arg Ile Ile Ser Thr Ser Ser
      130              135              140
Arg Ser Val Met Leu His Tyr Arg Ser Asp Leu Leu Gln Met Leu Asp
      145              150              155              160
Thr Leu Val Phe Ser Ser Leu Leu Leu Phe Gly Phe Ala Glu Gln Lys
      165              170              175
Gln Leu Leu Glu Val Glu Leu Tyr Ala Asp Tyr Arg Glu Asn Ser Tyr
      180              185              190
Val Pro Thr Thr Gly Ala Ile Ile Glu Ile His Ser Lys Arg Ile Gln
      195              200              205
Leu Tyr Gly Ala Tyr Leu Arg Ile His Ala His Phe Thr Gly Leu Arg
      210              215              220
Tyr Leu Leu Tyr Asn Phe Pro Met Thr Cys Ala Phe Ile Gly Val Ala
      225              230              235              240
Ser Asn Phe Thr Phe Leu Ser Val Ile Val Leu Phe Ser Tyr Met Gln
      245              250              255
Trp Val Trp Gly Gly Ile Trp Pro Arg His Arg Phe Ser Leu Gln Val
      260              265              270
Asn Ile Arg Lys Arg Asp Asn Ser Arg Lys Glu Val Gln Arg Arg Ile
      275              280              285
Ser Ala His Gln Pro Gly Pro Glu Gly Gln Glu Glu Ser Thr Pro Gln
      290              295              300
Ser Asp Val Thr Glu Asp Gly Glu Ser Pro Glu Asp Pro Ser Gly Thr
      305              310              315              320
Glu Val Ser Cys Pro Arg Arg Arg Asn Gln Ile Ser Ser Pro
      325              330

```

## (2) INFORMATION FOR SEQ ID NO:35:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: None

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

```

Met Thr His Pro Gly Thr Gly Asp Ile Ile Ala Val Met Ile Thr Glu
  1              5              10              15
Leu Arg Gly Lys Asp Ile Leu Ser Tyr Leu Glu Lys Asn Ile Ser Val
      20              25              30
Gln Met Thr Ile Ala Val Gly Thr Arg Met Pro Pro Lys Asn Phe Ser
      35              40              45
Arg Gly Ser Leu Val Phe Val Ser Ile Ser Phe Ile Val Leu Met Ile

```

50		55		60
Ile Ser Ser Ala Trp	Leu Ile Phe Tyr Phe	Ile Gln Lys Ile Arg Tyr		
65	70	75	80	
Thr Asn Ala Arg Asp	Arg Asn Gln Arg Arg	Leu Gly Asp Ala Ala Lys		
	85	90	95	
Lys Ala Ile Ser Lys	Leu Thr Thr Arg Thr	Val Lys Lys Gly Asp Lys		
	100	105	110	
Glu Thr Asp Pro Asp	Phe Asp His Cys Ala	Val Cys Ile Glu Ser Tyr		
	115	120	125	
Lys Gln Asn Asp Val	Val Arg Ile Leu Pro	Cys Lys His Val Phe His		
	130	135	140	
Lys Ser Cys Val Asp	Pro Trp Leu Ser Glu	His Cys Thr Cys Pro Met		
	145	150	155	160
Cys Lys Leu Asn Ile	Leu Lys Ala Leu Gly	Ile Val Pro Asn Leu Pro		
	165	170	175	
Cys Thr Asp Asn Val	Ala Phe Asp Met Glu	Arg Leu Thr Arg Thr Gln		
	180	185	190	
Ala Val Asn Arg Arg	Ser Ala Leu Gly Asp	Leu Ala Gly Asp Asn Ser		
	195	200	205	
Leu Gly Leu Glu Pro	Leu Arg Thr Ser Gly	Ile Ser Pro Leu Pro Gln		
	210	215	220	
Asp Gly Glu Leu Thr	Pro Arg Thr Gly Glu	Ile Asn Ile Ala Val Thr		
	225	230	235	240
Lys Glu Trp Phe Ile	Ile Ala Ser Phe Gly	Leu Leu Ser Ala Leu Thr		
	245	250	255	
Leu Cys Tyr Met Ile	Ile Arg Ala Thr Ala	Ser Leu Asn Ala Asn Glu		
	260	265	270	
Val Glu Trp Phe				
	275			

## (2) INFORMATION FOR SEQ ID NO:36:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: None

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Met Ala Asn Ser Gly	Leu Gln Leu Leu Gly	Phe Ser Met Ala Leu Leu
1	5	10
Gly Trp Val Gly	Leu Val Ala Cys Thr	Ala Ile Pro Gln Trp Gln Met
	20	25
Ser Ser Tyr Ala Gly	Asp Asn Ile Thr Ala	Gln Ala Met Tyr Lys
	35	40
Gly Leu Trp Met Asp	Cys Val Thr Gln Ser Thr	Gly Met Met Ser Cys
	50	55
Lys Met Tyr Asp Ser	Val Leu Ala Leu Ser	Ala Ala Leu Gln Ala Thr
	65	70
Arg Ala Leu Met Val	Val Ser Leu Val Leu	Gly Phe Leu Ala Met Phe
	85	90
Val Ala Thr Met Gly	Met Lys Cys Thr Arg	Cys Gly Gly Asp Asp Lys
	100	105
Val Lys Lys Ala Arg	Ile Ala Met Gly Gly	Gly Ile Ile Phe Ile Val
		110

(2) INFORMATION FOR SEO ID NO:37:

(A) LENGTH: 476 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Met 1	Ile	Arg	Pro	Gln 5	Leu	Arg	Thr	Ala	Gly 10	Leu	Gly	Arg	Cys	Leu 15	
Pro	Gly	Leu	Leu	Leu	Leu	Leu	Val	Pro	Val	Leu	Trp	Ala	Gly 30	Ala	Glu
			20					25							
Lys	Leu	His	Thr	Gln	Pro	Ser	Cys	Pro	Ala	Val	Cys	Gln	Pro	Thr	Arg
		35					40					45			
Cys	Pro	Ala	Leu	Pro	Thr	Cys	Ala	Leu	Gly	Thr	Thr	Pro	Val	Phe	Asp
	50					55					60				
Leu	Cys	Arg	Cys	Cys	Arg	Val	Cys	Pro	Ala	Ala	Glu	Arg	Glu	Val	Cys
65					70					75					80
Gly	Gly	Ala	Gln	Gly	Gln	Pro	Cys	Ala	Pro	Gly	Leu	Gln	Cys	Leu	Gln
				85					90					95	
Pro	Leu	Arg	Pro	Gly	Phe	Pro	Ser	Thr	Cys	Gly	Cys	Pro	Thr	Leu	Gly
			100					105					110		
Gly	Ala	Val	Cys	Gly	Ser	Asp	Arg	Arg	Thr	Tyr	Pro	Ser	Met	Cys	Ala
		115					120					125			
Leu	Arg	Ala	Glu	Asn	Arg	Ala	Ala	Arg	Arg	Leu	Gly	Lys	Val	Pro	Ala
	130					135					140				
Val	Pro	Val	Gln	Trp	Gly	Asn	Cys	Gly	Asp	Thr	Gly	Thr	Arg	Ser	Ala
145				150						155					160
Gly	Pro	Leu	Arg	Arg	Asn	Tyr	Asn	Phe	Ile	Ala	Ala	Val	Val	Glu	Lys
				165					170					175	
Val	Ala	Pro	Ser	Val	Val	His	Val	Gln	Leu	Trp	Gly	Arg	Leu	Leu	His
			180					185					190		
Gly	Ser	Arg	Leu	Val	Pro	Val	Tyr	Ser	Gly	Ser	Gly	Phe	Ile	Val	Ser
		195					200					205			
Glu	Asp	Gly	Leu	Ile	Ile	Thr	Asn	Ala	His	Val	Val	Arg	Asn	Gln	Gln
	210					215					220				
Trp	Ile	Glu	Val	Val	Leu	Gln	Asn	Gly	Ala	Arg	Tyr	Glu	Ala	Val	Val
225					230					235					240
Lys	Asp	Ile	Asp	Leu	Lys	Leu	Asp	Leu	Ala	Val	Ile	Lys	Ile	Glu	Ser

```

                245                250                255
Asn Ala Glu Leu Pro Val Leu Met Leu Gly Arg Ser Ser Asp Leu Arg
                260                265                270
Ala Gly Glu Phe Val Val Ala Leu Gly Ser Pro Phe Ser Leu Gln Asn
                275                280                285
Thr Ala Thr Ala Gly Ile Val Ser Thr Lys Gln Arg Gly Gly Lys Glu
                290                295                300
Leu Gly Met Lys Asp Ser Asp Met Asp Tyr Val Gln Ile Asp Ala Thr
305                310                315                320
Ile Asn Tyr Gly Asn Ser Gly Gly Pro Leu Val Asn Leu Asp Gly Asp
                325                330                335
Val Ile Gly Val Asn Ser Leu Arg Val Thr Asp Gly Ile Ser Phe Ala
                340                345                350
Ile Pro Ser Asp Arg Val Arg Gln Phe Leu Ala Glu Tyr His Glu His
                355                360                365
Gln Met Lys Gly Lys Ala Phe Ser Asn Lys Lys Tyr Leu Gly Leu Gln
370                375                380
Met Leu Ser Leu Thr Val Pro Leu Ser Glu Glu Leu Lys Met His Tyr
385                390                395                400
Pro Asp Phe Pro Asp Val Ser Ser Gly Val Tyr Val Cys Lys Val Val
                405                410                415
Glu Gly Thr Ala Ala Gln Ser Ser Gly Leu Arg Asp His Asp Val Ile
                420                425                430
Val Asn Ile Asn Gly Lys Pro Ile Thr Thr Thr Thr Asp Val Val Lys
435                440                445
Ala Leu Asp Ser Asp Ser Leu Ser Met Ala Val Leu Arg Gly Lys Asp
450                455                460
Asn Leu Leu Leu Thr Val Ile Pro Glu Thr Ile Asn
465                470                475

```

## (2) INFORMATION FOR SEQ ID NO:38:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: None

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

```

Met Val Lys Val Thr Phe Asn Ser Ala Leu Ala Gln Lys Glu Ala Lys
 1                5                10                15
Lys Asp Glu Pro Glu Ser Gly Glu Glu Ala Leu Ile Ile Pro Pro Asp
                20                25                30
Ala Val Ala Val Asp Cys Lys Asp Pro Asp Asp Val Val Pro Val Gly
                35                40                45
Gln Arg Arg Ala Trp Cys Trp Cys Met Cys Phe Gly Leu Ala Phe Met
50                55                60
Leu Ala Gly Val Ile Leu Gly Gly Ala Tyr Leu Tyr Lys Tyr Phe Ala
65                70                75                80
Leu Gln Pro Asp Asp Val Tyr Tyr Cys Gly Ile Lys Tyr Ile Lys Asp
                85                90                95
Asp Val Ile Leu Asn Glu Pro Ser Ala Asp Ala Pro Ala Ala Leu Tyr
100                105                110
Gln Thr Ile Glu Glu Asn Ile Lys Ile Phe Glu Glu Glu Glu Val Glu

```

		115				120				125					
Phe	Ile	Ser	Val	Pro	Val	Pro	Glu	Phe	Ala	Asp	Ser	Asp	Pro	Ala	Asn
	130					135					140				
Ile	Val	His	Asp	Phe	Asn	Lys	Lys	Leu	Thr	Ala	Tyr	Leu	Asp	Leu	Asn
145					150					155					160
Leu	Asp	Lys	Cys	Tyr	Val	Ile	Pro	Leu	Asn	Thr	Ser	Ile	Val	Met	Pro
			165						170					175	
Pro	Arg	Asn	Leu	Leu	Glu	Leu	Leu	Ile	Asn	Ile	Lys	Ala	Gly	Thr	Tyr
		180						185					190		
Leu	Pro	Gln	Ser	Tyr	Leu	Ile	His	Glu	His	Met	Val	Ile	Thr	Asp	Arg
	195						200					205			
Ile	Glu	Asn	Ile	Asp	His	Leu	Gly	Phe	Phe	Ile	Tyr	Arg	Leu	Cys	His
	210					215					220				
Asp	Lys	Glu	Thr	Tyr	Lys	Leu	Gln	Arg	Arg	Glu	Thr	Ile	Lys	Gly	Ile
225					230					235					240
Gln	Lys	Arg	Glu	Ala	Ser	Asn	Cys	Phe	Ala	Ile	Arg	His	Phe	Glu	Asn
			245					250						255	
Lys	Phe	Ala	Val	Glu	Thr	Leu	Ile	Cys	Ser						
			260					265							

115  
 130  
 145  
 165  
 180  
 195  
 210  
 225  
 245  
 260